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Art Unit: 1645

Thursday, June 19, 2003

Case Serial Number: 674277

From: Paul Schulwitz

Location: Biotech-Chem Library

CM1-6B06

Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

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Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (703)305-1954



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From: Sent:

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Sunday, June 08, 2003 10:49 AM STIC-Biotech/ChemLib

To:

Subject:

Sequence search 09/674,277

Importance:

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JUN - 9 2003

(STIC)

In re: 09/674,277

Please search SEQ ID NO:1 and 2. Please include and interference and commercial database search. Please print out top 50 hits in each category.

Thanks, Patricia A. Duffy CM1-8D05 AU 1645 703-305-7555

Searcher:
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Location:
Date Picked Up: 4//0
Date Completed: 6/19
Searcher Prep/Review:
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Online time:

TYPE OF SEARCH:
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AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
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VENDOR/COST (where	applic.)
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DIALOG:	
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WWW/Internet:	
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GenCore version 5.1.6

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cencore version 3.1.0 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	on: June 17, 2003, 15:59:59; Search time 2128.45 Seconds (without alignments) 16148.066 Million cell updates/sec	Title: US-09-674-277-2 Perfect score: 1181 Sequence: 1 ctgcaggagatggaaaaaaattttactttttctctgcag 1181	ng table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 2054640 segs, 14551402878 residues	number of hits satisfying chosen parameters: 4109280	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries	GenEmbl:* 1: qb.ba:* 2: qb.ba:* 4: qb.con:* 5: qb.cov:* 6: qb.pa:* 7: qb.pa:* 10: qb.pa:* 11: qb.sa:* 11: qb.sa:* 12: qb.ba:* 13: qb.un:* 14: qb.un:* 15: qb.un:* 16: qb.un:* 17: qb.un:* 18: qb.un:*	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description					AX191727 Sequence				AL391753 Shigella					AF326/// Snigella	AX100832 Secuence	L47709 Bacillus su	299115 Bacillus su	AE003927 Xylella f	AEUU/U/U Mycobacte	AF498417 PSeudomon	AF035937 Pseudomon	AP003599 Nostoc sp	AE008327 Agrobacte	AE009263 Agrobacte	AE013034 Thermoana	AC005674 Homo sapi	AX433280 Sequence	AP000007 Pyrococu	AL391406 Streptomy	AC092541 Homo sapi	AE012967 Chlorobiu	AX437696 Sequence	AE004745 Pseudomon	AEUUUBUS Methanoba AF498404 Psendomon	AP005369 Thermosyn	AE000469 Escherich	CONTINUATION (20 O	AC023609 Mus muscu	AC078885 Mus muscu	AF429315 HOMO Sapi	AE005627 Escherich		Ď.	AECOL/35 Thermolog) 뇠	L78814 Mycobacteri	AL022602 Mycobacte	ALS83920 Mycobacte	AP005370 Thermosyn	AF112861 Escherich	AE008892 Salmonell AL627279 Salmonell	1 6	AX433356 Sequence
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Submitted (14-FEB-1997) W. Brunder, Universitaet Wuerzburg,
Institut fuer Hygiene und Mikrobiologie, Josef-Schneider-Strasse 2,
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msbB gene; unidentified
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NYAPARDONSLAFWKFAGSGILEPHPREGOSQPHITSTERSLLLYPRYKADDKTP
VQVBARDDNNKILGTLTLYPPSSLPDTIYHLGVYPEGGIDFTPHNGTKKIINYVAEVN
KLSDASGSSIHSHLTNNALVEIHTANGRWYRDIYLPQGPDLEGKMVRFVSSAGYSSTV
FYGDRVLTSVGNTLLFKYVRGOWFRGELENNRITYAQHIWSAELFAHWIVPGLNLV
FYGGNLSGRLNDIKIGAPGELLLHTDIGMLTTP"
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Pred. No. 0;
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'db_xref="GI:4127817"
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1150 1736 2816 2696 2576 ö PAT 15-AUG-2001 130 250 70 Enterobacteriaceae; TGGAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAGTAGGCC CTCCGTTACCGGAAAACCGCTGAACAAATTCGGGCTGAAAAGAGGATCCGCCGTTATCT CAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTTTGTCTGACAAT TGGAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAGTAGGCC TGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAATGTGATAAATTA CTCCGTTACCGGAAAACCGCTGAACAAATTCGGGCTGAAAAGAGAGGATCCGCCGTTATCT GTTGCATTTCCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAAT **ATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGTCTGAGGATGGA AGGAAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACATCATGCCCTCTTTTTTCTGGC AGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTGTCATGGCCACT** Gaps ö Length 7395; and composition 3; Indels linear gamma subdivision; . 9 DB DNA TTCCGGAGCAATTTTACTTTTTCTCTGCAG 1181 TICCGGAGCAATTTTACTTTTTTCTCTGCAG 1705 Antisense antibacterial cell division Patent: WO 0149775-A 10 12-JUL-2001; Avi Biopharma, Inc. (US) /organism="Escherichia coli" /db_xref="taxon:562" | 1575 c 1815 g 2076 t Score 1166.2; Pred. No. 0; 0; Mismatches 7395 bp from Patent W00149775. Biopharma, Inc. (US) Location/Qualifiers Bacteria; Proteobacteria; Ax191728 Sequence 10 from Patent Ax191728 AX191728.1 GI:15209897 Query Match 98.7%; Best Local Similarity 99.7%; Matches 1168; Conservative Escherichia. 1 (bases 1 to 7395) co11 co11

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/db_xref="G1:3822115"
/translation="WAEQKRPVLTLKRKTEGETPVRSRKTIINVT#PPKWKVKKQKLA
ERAREABLAAKKAQARQALSIYLNLPTQDEAVNTLKPWPGLEDGDTPRLLAGGIRD
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YAAARLDKIFRQNRIKAELQAVLDEK"
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Protein_id="AAC70071.1"
/db_xref="GI:3822117"
/translation="MRKYIPLVFIFSWPVLCADIHGRVVRVLDGDTIEVMDSRKAVR
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QFWVRAGAAWVYEQYNTDPVLQNEARQQKRGLWSDADPVPPWIWRHRK"
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1658. 1867
/gene="L7004"
/note="55 pct identical (0 gaps) to 66 residues of
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/note="predicted sigma 70 promoter; score of 52%"
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    Acids Res. 26 (18), 4196-4204 (1998)
                                                                                                                                                                                               /serotype="0157:H7"
/db_xref="taxon:83334"
/lab_host="Escherichia coli C600"
/plasmid="P0157"
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Burland, V., Shao, Y., Perna, N.T., Plur
Blattner, F.R.
Direct Submission
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Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
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'db_xref="GI:3822116"
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approx. 269 aa protein E
/codon_start=1
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/product="hypothetical
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/note="predicted
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/gene="fino"
/note="L7001"
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/gene="L7002"
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TTCACGCCCGCCCCACCACGAGCCAGCGAAATGATTTCCCTTCCATCTTCAGCTGATA
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                                                            GGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGG
                                                                                                                         CATGACCACCACCACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGGGCCACCTGCCAT
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Burland, V., Shao, Y., Perna, N.T., Plunkett, G., Sofia, H.J. and
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Escherichia coli 0157:H7 plasmid po157, complete sequence.
AF074613.1 GI:3822114
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Escherichia coli 0157:H7
Bacteria; Proteobacteria;
Escherichia.
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ACCESSION
VERSION
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SOURCE
ORGANISM
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AF074613/c
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AUTHORS
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/ULTAINSTALLOISOKAILZA
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LATESAGKIGITRAPARALFEEEDITYOTEVPEIGGITPETPALEALEAGE
LATESAGKIGITRAPRALFEEEDIGITYOTEVPEIGGITPETPALEALEADV
SEDNVAAARRSRVEWENNIKKOGITREISEGRFTANRERVRERFRSYQTELKSRGIK
RARARDAGRERODIVILVKROLTREISEGRFTANREAVRREVERRFRSYGTELKSRGIK
YSRLAARSP
3847. .4095
/standard_name="CIS"
/note="88 pct identical to locus ECCIS accession X12587,
required for cis-activation of oriR by the replication
initation protein"
4072. .4080
/note="data site; 100 pct identical (0 gaps) to locus
ECNRIREP at (1682. .1690) accession X02302"
/standard_name="oriR"
/note="89 pct identical to oriR (1094. .1242); minimum
segment for replication of E. coli IncFil plasmid NRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19124 TCGGGATAAAAATCGCGCAGTGCGCGGTCCATGCAGAGACACATCCCCCACGGGTAACAG 19065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="95 pct identical to (0 gaps) 64 residues of a 128 as protein REPA4 locus ECRSC1 accession V00351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 IGTICTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAATGTGATAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGCATTTCCCCTTAGCCTGACTGAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19244 GITGCATTICCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 TCGGGATAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="'96 pct identical amino acid sequence and equal
length to REP2_ECOLI SW: P03066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 TGGAAAAAAAGCCAAAATAAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAGTAGGCC
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/note="predicted sigma 70 promoter; score of
4259. 4453
                                                                                                                                               /product="replication initiation protein"
/protein_id="AAC70076.1"
/db_xref="GI:3822122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.7%; Score 1166.2; 99.7%; Pred. No. 0;
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                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /direction=right 4169. .4197
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/transl_table=11
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/gene="L7009"
4259. .4453
/gene="L7009"
                         3040. .3897
/gene="rep2"
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Matches 1168;
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Anote="100 pct identical (0 gaps) to RBS at 641. .644 locus
ECNRIREP accession X02302"
                                                                                              /protein_1d="AAC70072.1"
/db_xref="GI:3822118"
/translation="MEKTKQEWLYQLRRCSSVNTLEKIIHKNRDSLSTSERESFNSAA
                                                                                                                                                                                                                                                                                                                                                                                                              /product-"hypothetical protein"
/protein_id-"AAC70073.1"
/db_xref-"GI:3822113
/translation-"WrilifiliviliaalLirriliksynOHSPLLWQLHAAGIRTGD
AERILSGGEYDASHLRPERRRRDILLEEVLRQAGIPLLRSHDARKLLQWTGEWINTTG
                                                                                                                                                                                                                                                                                                         /note="98 pct identical (0 gaps) to 57 residues of an approx. 200 as protein; plasmid R100 miniplasmid pSM1 ORF 4, TRSW: Q52340"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ssiB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="91 pct identical (0 gaps) to 24 residues of an approx. 24 aa protein uORF P3OREPFIC, accession M16167, translationally coupled to replication initiation protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MSQTENAVTSSSGAKRAYRKGNPLSDAEKQRLSVARKRASFKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2473. .2478
//note="100 pct identical (0 gaps) to RBS at 80. .85 locus
ECKNRIERS accession X02302"
//gene="cpb2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="initiation site; Escherichia coli plasmid R100 sr
jene; 99 pct identical to ss1B locus R10SSIB accession
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length to CPB2_ECOLI SW: P03847"
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                                                                                                                                                                      2754. .2782
/note="predicted sigma 70 promoter; score of 69%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2416. .2421

/note="100 pct identical (0 gaps) to the -35

2439. .2445

/note="100 pct identical (0 gaps) to the -10

/note="100 pct identical (0 gaps) to the -10

2473. .2478
  P23870"
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/protein_ld="AAC70075.1"

/db_ref="GI:3822121"

/translation="MIGKVQDFFLCSLLLRIVSAGWCD"
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Protein_id="AAC70074.1"
'db_xref="G1:3822120"
72 aa protein HHA_ECOLI SW:
                                                                                                                                                                DHRLAELITGKLYDRIPKEIWKYVR"
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                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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/transl_table=11
                                                                                                                                                                                                                            1905. .2243
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1905. .2243
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2483. .2737
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/gene="rep2"
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BASE COUNT 24693 a 20133 c 23728 g 23523 t	Query Match 98.7%; Score 1166.2; DB 6; Length 92077; Best Local Similarity 99.7%; Pred. No. 0; Matches 1168; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	QY 11 TGGAAAAAAGCCAAAATAAAAATTGCCCATCCCAGGGCGCTCCAGGTGAAAGTAGGCC 70 	OY 71 TGTTCTGTCCGGTATTTAAATGCCATTGACCGTCCCCGTATTTAAACAATGTGATAAATA 130 	OY 131 CTCCGTTACCGGAAAACCGCTGAACAAATTCGGGCTGAAAAGGGATCCGCGTTATCT 190 19304 CTCCGTTACCGGAAAACCGCTGAACAAATTCGGGCTGAAAAGAGGATCCGCCGTTATCT 19245	QY 191 GTTGCATTTCCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAAT 250	QY 251 ATCAAACGGTACTCAATATCTTCTGGGGCTGCCTGCCATCATCAGGGAGGG	OY 311 TCGGGATAAAAATCGCGCAGTGCGCGGTCCATGCAGACACATCCCCCACGGGTAACAG 370	OY 371 CGTCCTGTCACATTCTTCTGAATGACATCCGGCCCGCCCG	QY 431 GGGCACGCGGAGACTGACGCTTCAGCCAGTACCAAACGCTTCATTTCCGAAGG 490	QY 491 CATGACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGGGCACCTGCCAT 550 	QY 551 TAACACATCTCCGCTCATTCCCAGGTGTTCTGTCGCTGCTGCAGACGTGCTTCGTATTC 610	OY 611 TTCACGCCCGCCCCACCACCAGCGAAATGATTCCCTTCCATTTAGGTGATA 670	OY 671 CAATACACGCAGCATAAATTCATGTCCTTTTTCGGGACGTAGCATCCCCACCTGAACGAT 730	Qy 731 AAGCGGAACATTGTCTGCTGATGCCGGCGTGGATATGCAGGGGTAACGGTCGCAT 790	QY 791 GGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAATAACCGTTACCGGTGTCCT 850	OY 851 GACACCTTCGCCATCAGATGCGCCATCATGGCTGAGATAGGCACAACAATGAAATCACA 910		Qy 971 AGTGAAGCGGTGACAGCATATCAGACGGCTCAGCTGCTGTATACTGTCATGGCCCT 1030
490	19004	551 TAACACATCTCCGCTCATTCCCAGGTGTTCTGCTGCGACGAGGTTCGCTACGTATTC 11+	611 TTCACGCCGGCGCCCACCACGAGCCAAATGATTCCCTTCCACCTCAGCTGATA 1111111111111111111111111111111111	730	CAT CAT	CCT 850 CCT 1858	Qy 851 GACACCTTCCGCCATCAGATGCGCCATCATGGGTGACATAGGCACAACAATGAAATCACA 910 1		AGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTGTCATGGCCACT	1031 ATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGTCTGAGGATGGA 18404 ATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGATCAGGATGAGATGA	AGGAAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACATCATGCCCTCTTTTTCTGGC 1150			ANISTICATOR ANISTRA LOCUS DEFINITION Sequence 9 from Patent W00149775. ACCESSION ANISTRA VERSTON ANISTRAL OF ANISTRAL ANISTRAL ANISTRAL OF	RDS SE Escherichia coli. SANISM Escherichia coli	Backerla; Proteobacteria; gamma subdivision; Enterobacteria Escherichia. CE 1 (bases 1 to 92077) RS Iversen, P.L.	Antisense an Patent: WO C Avi Biopharm	source 1yzv/. /organism="Escherichia coli" /db_xref="taxon:562"

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                                                                                                                           on Apr 20, 1999 this sequence version replaced g1:3336997.

Location/Qualifiers

1. 92721

f. 1972

f. 1973

f. 2015

f.
18464 ACTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTGTCATGGCCACT 18405
                                                                                                                                                                                                                                                      1150
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STAGLGENSHPYVVAOLAAHNSRGNYANGIQVHGGSGGGGIVTLDSTLGNEFSHEVGH
NYGLGHYVDGFKGSVHRSAENNNSTWGWDGDKKRFIPNFYPSQTNEKSCLNNQCQEPF
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/translation="MNTKMNERWRTPMKLKYLSCTILAPLAIGVFSATAADNNSAIYF
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VQVEARDDNNKILGTLTLXPPSSLPDTIYHLDGVPEGGIDFTPHNGTKKIINTVAEVN
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IKQGNLSGRLNDIKIGAPGELLLHTIDİGMLTTPRDRFPFAKDKEAHREYFQTIPVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB011549 92721 bp DNA circular BCT 27-APR-1999 Escherichia coli plasmid pol57 DNA, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Makino, K., Ishii, K., Yasunaga, T., Hattori, M., Yokoyama, K., Yutsudo, H.C., Kubota, Y., Yamaichi, Y., Iida, T., Yamamoto, K., Honda, T., Han, C.G., Ohtsubo, E., Kasamatsu, M., Hayashi, T., Kuhara, S. and Shinagawa, H.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                      1091 AGGAAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACATCATGCCCTCTTTTTCTGGC
                                                                                        1031 ATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGTCTGAGGATGGA
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Submitted (24-FEB-1998) Kozo Makino, Research Institute for
Microbial Diseases, Osaka University, Molecular Microbiology;
yamadaoka, 3-1, Suita, Osaka 562, Japan
(E-mail:makino@bkns01.biken.osaka-u.ac.jp, Tel:81-6-879-8318,
Fax:81-6-879-8320)
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AB011549.2 GI:4589740
AB011549.2 GI:4589740
Escherichia coli (strain:0157:H7, sub_strain:RIMD 0509952)
plasmid:pol57 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18284 TTCCGGAGCAATTTTACTTTTTTCTCTGCAG 18254
                                                                                                                                                                                                                                                                                                                                                                                                                              TICCGGAGCAATTITACTITITICTCTGCAG 1181
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/gene="tagA"
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/product="Type II secretion pathway related protein"
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ATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGTCTGAGGATGGA 1090
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Oy 551 TAACACATCTCC Db 88399 TAACACATCTCC OY 611 TTCACGCCCGG Db 88339 TTCACGCCCGGC Oy 671 CAATACACCCC Db 88279 CAATACACCCCA	731 88219 791 88159 851 851	88039 971 87979 1031	Oy 1091 AGGAAGGTGAA Db 87859 AGGAAGGTGAA OY 1151 TTCCGGAGCAA Db 87799 TTCCGGAGCAA		REFERENCE I (bases I target and the locus an	MEDINE 98261495 PUBMED 9596716 REFERENCE 2 (DASSES I t AUTHORS BOCTLIN, P. an TITLE DIRECT SUDMIT JOURNAL SUDMITTEE (LAT
### ##################################	AXI99725 AXI91725 AXI91725 BY 2721 bp DNA linear PAT 15-AUG-2001 LOCUS Sequence 7 from Patent W00149775. DEFINITION Sequence 7 from Patent W00149775. VERSION AXI91725 GI:15209894 VERSION AXI91725.1 GI:15209894 VERSION	Avi Blopharma, Inc. (US) Avi Blopharma, Inc. (US) Incation/Qualiflers ree /organism-"bscherichia coli" /db_xref-"taxon:562" NT 24870 a 20267 c 23868 g 23716 t Match 98.7%; Score 1166.2; DB 6; Length 92721; coal Similarity 99.7%; Pred: No. 0;	O; AAAi AAAi ATG	131 CTCCGTTACCGGAAAACCGCTGAACAAAATTCGGGCTGAAAAGAGGATCCGCCGTTATCT 190		431 GGCCACGCGGAGACTGACGCTTCAGCCAGTACCAACGCTTCATTTTCCGAAGG 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown"
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/mrenaragesreptution="Millinglowepergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictopergrenestrictope
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GYDIPAMLMAASSKRAAMFHNQRNPVVDYWNSVRREGGKLHARNDGIASFVRSVR
QGYWGYYLPDQDHGFPEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WLVVGAGREEYEASLEQOTEHLGMSGTVLAMAGALFPALLPVRIADENDSTR
WLVVGAGREEYEASLEQOTEHLGMSGTVLAMAGALFPALLPVRIASVVVWPSEREAFGM
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VSRAEGCRLWKEDILVGRQCLTEKLGFCSSHLCWPEGYYNRDYINLAGKLGFGSTLYTT
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/serotype="0157:H7"
/db_xref="taxon:562"
/plasmid="pol57"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAC24351.1"
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                                                                                                                                                                                                                                                                                                                                                                                                 complement(751. .2499)
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                                                                                                                                                       complement(<1. .705)
/gene="ecf4"
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ORIGIN
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/traislation-"MMIDGYRPYCRIVNKKNESISDIAFAHIIKRVKNSSCTHPKAAL
VFLCEKGECCDSNDVLSIMGQIPRVFKNKMLYDVVFKNEKSKNDFLKMAESWLPOSEP
VLINDDDDALNAAAYFSVKRAKIKTVNDTDFKER NKVYLIGHGSPGSMLGGIGSELID
VQTIISRMCOGILMYKDIRFTSCGSADKVARNNAPAESLSCILMSLPFFKEKES
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SFGWAVALILABIHORRAELIARGYERGESRVICGAHWQSDVEAGRLAGASVVAULH
NTPEFTKSLSSEAKKEFEELNTPTNELTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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secretion machinery, function unknown"
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INHQMALGIKIRRVQESEKWYVQFFDPNRTVTHKRTVFTCDSHFELSQLSAKDFFDDF
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KNEBEISOSKIVNLLARTSSOFTPARTALOMOSTDIQVYGKILNMOKISOETILTL
LAAVGANNVPGLCMSERNGHYDTIRAYGEIVRKTPLTSDRRIYLTLARDSHDLPGLFF
ALONGHADSIRMFGSLLNKKMLSSEQIKELLKVKHGLFMALONGHTKAIMAYGDILKF
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TNKDGIPGVFVSVVNRDKETILEYCRIIKENNLEPDTIAEQFSKKMKKTFIEIINRFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5527. .5657
/note="IS629.02, 93% id over 130 nt with IS629, from 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7573. 7602
/note="IS630.01, 93% id over 30 nt with IS630, from 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ORF12, length= 239 aa, 63.3% id in 245 aa overlap
with STMKFA_1 (Salmonella typhimurium virulence plasmid
MKFA = 241 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="OR10, length= 569 aa, 39.7% id in 537 aa overlap
with ECSHET2B_1 (S. flexneri SenA 565 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="PhoN2 (Apy), periplasmic phosphatase, apyrase, ATP diphosphohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7603. .8111)
fnote="ISShf5.01, fragment of the putative ISShf5,
220 to 1732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                over 743 nt with IS600,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ospc4 gene, inactivated by frameshits"
7573. 7602
                                                                                                                                                                                                                                                                                                      4680. .5420
/gene="phoN2 (apy)"
4680. .5420
/gene="phoN2 (apy)"
/note="ORE5, PhoN2 (Apy), length= 246 aa,
SFU04539_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(11642. .12361)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1220 to 1732"
complement(8133. .8875)
/note="IS600.01, 91% id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5782, .7051)
                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                 QKKTFIINKELD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ospD2"
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  ATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCGTCGAAGTCTGAGGATGGA 1090
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1 to 213494.
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DKDWNNSNTPQVWTDQSWHPNTHLRDANEFELNLKGWLLNNLDYRLGLIAGYQESRYS
FNAMGGSYIYSENGGSRNKKGAHPSGERTIGYRQLFKIPYIGLTANYRHENFEFGAEL
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KAGPTSLYBOSTNIGSTIKNSASIEVIGFLTSAGIKVIF"
Complement(1975. .1128)
/note="18629.01, 95% id over 154 nt with 18629, from 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (Dases 1 to 213494)
Glaser,P., Buchrieser,C., Rusniok,C., Nedjari,H., d'Hauteville,H.,
Glaser,P., Sansonetti,P. and Parsot,C.
Direct Submission
Submitted (29-AUG-2000) P. Glaser, Institut Pasteur, Genomique des
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
Cedex 15, FRANCE. E-mail: pglaser@pasteur.fr Phone: +33 1 45 68 89
J6, Fax: +33 (0)1 45 68 87 46
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96% id over 385 nt with IS2, from 1 to 393"
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Bubriaceser, C., Glaser, P., Rusniok, C., Nedjari, H., D'Hauteville, H., Runst, F., Sansonetti, P. and Parsot, C. The virulence plasmid pWR100 and the repertoire of proteins secreted by the type III secretion apparatus of Shigella flexneri MG1. Microbiol. 38 (4), 760-771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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family, involved in cleavage of surface exposed IcsA"
/dp_tretin_id="CACO5766.2"
/db_xref="GI:12329038"
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/gene="icsP (sopA)"
/note="ORF1, IcsP (SopA), length= 315 aa, id
and AF0016 33_1"
                                                                                                                                                                                                                                                                                                                                             Shigella flexneri virulence plasmid pWR100: from 1 AL391753.1 GI:12329037 virulence plasmid, type III secretion. Shigella flexneri. Bacteria neers
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/organism="Shigella flexneri"

/strain="M90T"

/db_xref="taxon:623"

/gene="icsp" (sopA)"

991. .1938
                                                                                                                                                                                            /gene="ospB"
/note="ORF4, length= 288 aa"
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/note="IS2.01, 9
3485. .4351
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3485. .4351
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AUTHORS
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PUBMED
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187295 TGCTTCGCTAATGTGAGTATTTTAACGCAGTTTTATTAATAATCAAACCGCTCTTCTATA 187236
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                                                                                                    187235 TCCTGTTTTGCCTGGCGAGCCATCTGATAAAAACGCCCAGGGTCATTAAAAAATCATTC
                                                                                                                                                                                                                                                                                                                                                    690 TCATGTCCTTTTTCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAACATTGTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    750 GATGCAGCCCAGGCGTGGATATGCAGGGTAACGGTCGCATGGCTTCATTATGCAATGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               870 TGCGCCATCATGGGTGAGATAGGCACAACAATGAAATCACACAGATAATTCAGGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 GTTCTGGTCTTACGGGTGATGTAGGTTTTTTGTCTGACAATAGTGAAGCGGTG---ACAG
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                                                                                                                                         330 AGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTC
                                                                                                                                                                                                            390 TGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGAC
                                                                                                                                                                                                                                                                                  GCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACTGGCA
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 TGACTAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAATATCAAAACCGGTACTCAATA
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QYPAYYKVASNVPPYSDICQFFSYMYQGFOIVNHSGDVFHACRERPQSKGDFVGDK
HHISTAREQVPLAFQILSGLLFSEDSPIDKWKITDMRVSQQSRVGICAQFTLYVKSD
QECSQYSALLLHKIRQFIMCLESNLLRSKIAPGEYPASDVRPEDWRYVSYRNELRSDR
DGSERQEQMLREEPFYRLMIE*
                                                                                                                                                                                                                                          /protein_id="caco5774.1"
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/translation="MKVSFKSLGYIFHDIYNKHTIDEFNDVVRRAVLSGKINELNAC
HKYAIFLAEKDNEITKEKDKAKIIDTLTENYSIEFQOLMNISERTLNSLYIPPGESGF
VSFVNREGKICHTAYVKSSDNSMTYYHANGSSIDKYITDMCGLICMRHIESTGIIFYM
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/protein_id="cc0576.1"
/db_xref="GI:L2329045"
/translation="MLQRQRGKVGFAQLPVDFVAIEPDSVQGVGKRANLTNRCFIIRI
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AHAREKSGGGYSGYVSFRKLAKIONISIPTKNNEYNKHNHESHJHWFRYSE
SLLAAEIPREEKLEYLARNHAGESALFIALQEGHSAAIQAYGDEIKUPDLSPRETIK
LLDVRDNEGLPGELFLAAGKGNIEAMMAYINICHSGIKLTEIADRLNNNEQDMFNIIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84% id over 143 nt with IS630, from 999
                                                                                                                                                                                                                                                                                                                                                                                      complement(14367. .14629)
note=""IS21.01, 97% id over 263 nt with IS21, from 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(15925, 17350)
/note="ISA 01, 99% id over 1426 nt with ISA, from 1 to 17351, 19039
                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(14630 .15558)
/note="IS91.01, 97% id over 929 nt with IS91, from 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from 1130
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/product="OspDl, secreted by the Mxi-Spa secretion
machinery, function unknown"
/protein.id="CaCO5775.1"
/db_xref="G1:12329044"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Mxi-Spa secretion
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/note="ISShf5.02a, id_to_ISShf5 from 1 to 366"
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                                                                                                                                                                                                                                                                                                                                                    14014. .14241
/note="IS2.02, 90% id over 228.nt with
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                                                                                                                                                                    complement(13393, 13971)
/note="ORF13, length= 192 aa, unknown"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown"
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Pred. No. 1.4e-94;
0; Mismatches 394;
                                                                                                                                                                                                                                                                                                                                 LDEKVLSAIAEFMNEKGWRAAFCSAKNLYKCV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               id over 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF22,length = 104 aa,
              /product="oapF, secreted by
machinery, function unknown"
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/db_xref="GI:12329042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21977. .22105
/note="IS3.02, 89%
                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (14630.
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/note="IS630.02,
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/gene="ospD1"
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llarity 59.3%;
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	/strain	/db_xref="taxon:42897" /plasmid="pcP301" /insertion_seq="15629" /note="virulence plasmid" 167032167685 /organism="Shigella flexneri 2a" /strain="301" /db_xref="taxon:42897" /plasmid="pcP301" /insertion_seq="153128" /note="virulence plasmid" /complement(172967173339) /strain="301" /strain="301"	/db_xxef="taxon:42897" /plasmid="taxon:42897" /insertion_seq="%20-ISIN" /insertion_seq="%20-ISIN" /insertion_seq="%20-ISIN" 186968187636 /organism="Shigella flexneri 2a" /strain="301" /db_xxef="taxon:42897" /plasmid="pcP301" /insertion_seq="fs629" /ote="virulence plasmid" /complement(191493) /gene="CP0001" /gene="CP0001" /note="similar to a 301 aa protein from bacteriophage SfX gb: AAD10297.1"
source source source	source	source	source gene CDS
Shigella flexneri 2a strain 301 virulence plasmid pCP301, complete sequence. AF386526. AF386526.1 GI:18462515 Shigella flexneri 2a. Shigella flexneri 2a. Shigella flexneri 2a. Shigella flexneri 2a. Shigella flexneri 2a. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Shigella flexneri 2a. Jin, O., Zhang, J.Y., Liu, H., Yang, J., Yang, F., Zhang, X.B., Mang, J.H., Yang, G.W., Wu, H.T., Dong, J., Sun, L.L., Xue, Y., Zhao, Y.S., Zhu, J.P., Kan, B., Chen, S.X., Yao, Z.J., He, B.K., Chen, R.S., Man, D.L., Yuan, Z.H., Xu, J.G., Wang, Y., Shen, Y., Lu, W.C., Qiang, B.Q., Wen, Y.M. and Hou, Y.D., Wang, Y., Shen, Y., Lu, W.C., Chang, J.Y., Liu, H. T., Dong, J., Sun, L.L., Xue, Y., Ju, Q., Zhang, J.Y., Liu, H. T., Dong, J., Sun, L.L., Xue, Y., Zhao, A.L., Gao, Y.S., Zhu, J.P., Kan, B., Chen, S.X., Yao, Z.J., Wang, J.H., Yang, G.W., Wu, H.T., Dong, J., Sun, L.L., Xue, Y., Zho, J.P., Xan, B., Wang, J.H., Yang, G.W., Wu, H.T., Nan, B., Chen, S.X., Yao, Z.J., Lu, W.C., Qiang, B.Q., Wen, Y.M. and Hou, Y.D. Direct Submission of Warar Street Yang, B., Hang, H. Holl Health, Jon Yingxin, Street Yang, B., Hang, H. Hang, H. Hang, H. Hang, H. Hang, H. Hang, H. Hang, H. Hang, H. Hang, H. Hang,			e JOBOB. /Organism="Shigella flexneri 2a" /Strain="301" /Ab_xref="taxon:42897" /Insertion_seq="15829" /Insertion_seq="15829" /Organism="Shigella flexneri 2a" /Strain="301" /Ab_xref="taxon:42897" /Ab_xref="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAL72323.1"
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IVINNDDDALNAAAYFSVKRAKIKTVNDTDFKEYNKVYILGHGSPGSHQLGIGSELID
VGTITSRRMCGGILNYKDIRFTSCGSADKVARKNNNAPAESLSCILNSLPFKEKES
LLEOIKKHLENDESLSDGLKISGYHGYGYHYGQELFPYSHYRSTSIPADPEHTVKRSS
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SGRRSSSYLAQLRDVSARGDAVKNGRTLPEQDSGLPALVSDPGLPRMISTVL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389
                                                                                                                                                                                                                                                                                                                                                                                                      //note-"similar to a 288 aa protein from Shigella flexneriemb: CAC05770.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 TGACTAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAATATCAAACCGGTACTCAATA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGAC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aa protein from Shigella flexneri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCTCGGCGCTGCCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTC
                                                                                                                                                                   /note="similar to a 333 aa protein from Sphingomonas
3b: AAD45420.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 221618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.8%; Score 328.6; DB 1;
larity 59.3%; Pred. No. 1.4e-94;
Conservative 0; Mismatches 394;
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                                                                                                                                                                                                                                 /product-"hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to
jb: AAA21206.1"
                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
/codon_start=1
/transl_table=11
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                                                                                                         185. .949
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                                                                                                                                      485. .949
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                                                                                                                                                                                                                                                                                                                                                         /note="CP0003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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/gene="apy"
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Matches 57
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193275 CCCATACTGTCAATCTGAAATGCTCCCGCAGTTCAGGCGAACCAGACCCACA 193216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193395 GCTTCTGCCAGTACCATACCAAACGATTCGTTTTCTGAAGGCAGAACCACCAGACTGGCA 193336
                                                                                            193276
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                                                   569
                                                                                                                                                                                                                                         689
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Burland, V. and Blattner, F.R.
Complete DNA sequence and analysis of the large virulence plasmid
of Shigella flexneri
Infect. Immun. 69 (5), 3271-3285 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shigella flexneri
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               570 CCCAGGIGITCIGICIGCIGACGCAGACGIGCITCGIAITCITCACGCCCGGCGCCCACC
                                                                                                                                                                                                                                  630 ACGAGCCAGCGAAATGATTTCCCTTCCATCTTCAGCTGATACAATACACGCAGCATAAAT
                                                                                                                                                                                                                                                            690 TCATGTCCTTTTTCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAACATTGTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                        750 GATGCAGCCCAGGCGTGGATATGCAGGGTAACGGTCGCATGGCTTCATTATGCAATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193095 GACGCCAGCCAAGAAGAACATTTGGAGGCAAACTGTTTCGGGAATCAACGTATAATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870 TGCGCCATCATGGGTGAGATAGGCACAATGAAATCACACAGATAATTCAGGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 GTTCTGGTCTTACGGGTGATGTAGGTTTTTTGTCTGACAATAGTGAAGCGGTG---ACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATATCAGACGCTCAGTCCTGCTATATTACTGTCATGGCCACTATGGCAGATGACCAGA
                                                ATCCGGTAGACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGCTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF348706 221851 bp
Shigella flexneri large virulence
sequence.
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SFGWAPALILAEINPORKABILERGYERGESRYICGAHWQSDYEAGRLMGASVYAVLH
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complement(3470. 44441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="S0006"
/note="residues 8 to 285 of 323 are 22.56 pct identical to residues 56 to 301 of 612 of product encoded by GenBank accession Number AL008970), Hypothetical protein, len: 613 /codon_start=1 //transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"mikfslkiykhirihtlrilkkslftilfegveisnhoekleln
kthhyvyfganaxiidhdspygymtltehfdnaippyfyhehgsffldnfkevvdevs
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ktyequeytippytspwkriklrisdisledaikasnyeeinnkytdkmahgalays
ligdkradiallilskiptykodyaemekmnniychlyddytlsgrocanykueyfi
nwglydvnkkfogransgdymldnamkskdskmidffikkwsgirgti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="residues 38 to 128 of 132 are 23.15 pct identical to residues 41 to 123 of 839 of product encoded by GenBank Accession Number 299115 yon0 [Bacillus subtilis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="wknelkksiaaosyskwpsogtsfkslulsieapsgarssfrsl
EHLDKVSRHYISEIIQKVHPLSSDERHLLSIIINSNFNFRHQSNSNLSNNILNIKSFD
KIQSENIQTHKNTYSEDIKEISNHDFVFWG"
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SALQEEMAETLGEQYDPVLPSSLRQSSARKPLPASLPRAPRVIRPEEECCPACGGELS
PLGCDVSEQLELISSAFKVIEKQRPKLACRRCDHIVQAPVPSKPIARSYAGAGLLAHV
                                                                                                                                                                                                                                                                                                              /note="residues 27 to 59 of 84 are 36.36 pct identical to residues 427 to 459 of 729 of product encoded by GenBank Accession Number D63999 hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="residues 5 to 177 of 183 are 94.21 pct identical residues 42 to 214 of 523 of product encoded by GenBank Accession Number AB024946 orf51 [Escherichia col1]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="ISEc8 orf, fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="orf, hypothetical"
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complement(5742. .6164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4344. .4742)
/gene="S0007"
complement(4344. .4742)
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/gene="S0008"
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                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp.]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                  3272. .3526
/gene="S0005"
3272. .3526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                               3272. .3526
/gene="S0005"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485. 949
//gene="80002"
/note="residues 13 to 93 of 154 are 40.74 pct identical to
residues 5 to 85 of 333 of product encoded by GenBank
Accession Number U65001 putative resolvase [Sphingomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="residues 20 to 100 of 100 are 88.23 pct identical to residues 217 to 301 of 301 of product encoded by GenBank Accession Number AE000291 IS2 hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="IS2 orf2, fragment"
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1176. . 2042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="residues 130 to 273 of 288 are 28.57 pct identical to residues 12 to 139 of 340 of product encoded by GenBank Accession Number AL139075 ketol-acid reductoisomerase [Campylobacter jejuni]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MNLDGVRPYCRIVNKKNESISDIAFAHIIKRVKNSSCTHPKAAL
                             2 (bases 1 to 221851)
Venkatesan, M.M., Goldberg, M.B., Rose, D.J., Grotbeck, E.J.,
Venkatesan, M.M., Goldberg, M.B., Rose, D.J., Grotbeck, E.J.,
Burland, V. and Blattner, F.R.
Direct Submission
Submitted (13-FEB-2001) Laboratory of Genetics, University of
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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/protein_id="AAK18313.1"
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/organism="Shigella flexneri"

/db_xref="taxon:623"

/plasmid="virulence plasmid pwR501"

/complement(191. .493)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [Escherichia coli]"
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/gene="S0004"
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     11292750
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  PUBMED
REFERENCE
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JOURNAL
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Czeczulin,J.R., Whittam,T.S., Henderson,I.R., Navarro-Garcia,F. and
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                      TCATGTCCTTTTTCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAACATTGTCTGCT
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Czeczulin, J.R., Whittam, T.R., Henderson, I.R. and Nataro, J.P. Direct Submission
Submitted (11-MAR-1999) Vaccine Development, Univ. of Maryla W. Baltimore St., Baltimore, MD 21201, USA
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/organism="Escherichia
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/db_xref="taxon:562"
/plasmid="pAA2"
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/gene="shf"
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                                                                                                                                  /product="153 orfb, fragment"
/protein_id="Aak18320.1"
/protein_id="Aak18320.1"
/db_xref="G1:13310496"
/translation="MCRVPGVSRSGYYDRVQHAPSDRKQSDERLKLEIKVAHIRTRET
YGTRRLQTELABNGITYGRDRLARLKELKLEKCKRKFRATTNSDHNLPVTPNLLNG
NFTPTAPNQVWVADSVVQAFRNQPTEGAGRETAAYAR"
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VTAARKGLNTPGSRTVAELESEVMQLRKALNEARLERDILKKATAYFAQESLKNTR"
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//octe="rsolules | to 58 of 105 are 34.48 pct identical to //octe="rsolules | to 58 of 105 are 34.48 pct identical to residues 383 to 437 of 1003 of product encoded by GenBank Accession Number ALO13835 similar to Src homology domain 3; cDNA EST yk491e6.5 comes from this gene; cDNA EST WAR555 comes from this gene; cDNA EST yk200b8.5 comes
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                                                   /note="residues 1 to 116 of 140 are 90.51 pct identical residues 1 to 116 of 272 of product encoded by GenBank Accession Number X05952 pot. ORF B [Shigella sonnei]"
                                                                                                                                                                                                                                                                                     /gene="s0010"
/note="residues 1 to 100 of 100 are 93.99 pct identical
residues 1 to 100 of 100 of product encoded by GenBank
Accession Number X05952 pot. ORF A [Shigella sonnel]"
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0; Mismatches 394; Indels
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/db_xref="GI:13310497"
/gene="S0009"
complement(5742. .6164)
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complement(6200. .6502)
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/product="ISEc8 orf"
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Nakata,N., Sasakawa,C., Okada,N., Tobe,T., Fukuda,I., Suzuki,T.,
Komatsu,K. and Yoshikawa,M.
Identification and characterization of virk, a virulence-associated
large plasmid gene essential for intercellular spreading of
Shigella flexneri
MOI Microbiol. 6 (16), 2387-2395 (1992)
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University of Tokyo
4-6-1 Shirokanedal, Minato-ku
Tokyo 108
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VVSIRYYYELBSLPOLEDILALHPILADRIHRFYLHKGGRAWTRGQTILEHYRRVQNL
PEKYSKELFPGKSSLJVGFIGKDGRAFDIQGSPGGFREGELMLSLFTWKTVLARLTY
SVILTONGHIAFIGGLGGAPKNTGPDVIRCATRACYGLFPKRIIFEAFCALMKACNVS
ECLAVSEHSHVFROLKYWYGRRTFYAVYSDFWDSVPGKTCGDWYKLPTQVIRKPLTD
IPPIKRSDSYRACYALLDYIHFTIHFTIAFSLGAYPVHSKHONSN"
668 C 800 g 1039 t
660 G 1039 t
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                                                                                                                                                                                                                                                                                                                                                                                                 /traislation-"MNILETESSPNIGGOELQAVAQMKALKKMGHSVLLVCRENSKIA
FEASKFGIDITFALFRNSLHIPTVMRLLGIVHSFQPDAIVCHSGHDSNIVGLVRFFTW
FHPFRIIRQKTYLTRRKYFFSINHFCDEVIVPGTSMYTHLEQEGCRTRVTVVPPGFDF
QELYVDSRNSLPPSYLSWILASRRGCPVIAQVGMLRPEKGGDPLCWLIVGFGLPELREH
LQYQIDSMGMHDDVFIADNVFLPPPYIGLPVWWFCLQKTNLLVWCWQKHRHFLCL"
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                                                                                                                     /translation-*MINGGGILEKANHUPVLMYHHVSHCPGIVTLSPETFRKQMKWLA
ENNWKTLSSDELEFFYRGGKLPRKSVMLTFDDGYLDNWFOVYPLLNEFULKAHVFLIT
STGNGVPWRISPGKEYSHNDCEHQIAHGNADLWMLRWSEVNEMLQSGIVVEFHVHTYH
TRWDKKTTSREEQOKHLRQDLIGSGREYLKKWGKCSKHLCKPEGYYNEDYIQTAEELG
FHYLYTTERRWNAPAKGAARIGRISTKERSCAWLKRHLFYYTTPFFSSLLALYKGPR
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                     similar to Shigella flexneri Shf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 TCTTCTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGC
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Pred. No. 3e-68;
0; Mismatches 379; Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="similar to Shigella flexneri VirK"
                                                                                                                                                                                                                                                                                                                                                product="hexosyltransferase homolog"
protein_id="AAD34405.1"
/db_xref="G1:4959585"
                                                                                                                                                                                                                                                                                                 'note="CapU; hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAD34406.1"
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                                                                                      /protein_id="AAD34404.1"
/db_xref="GI:4959584"
       'gene="shf"
'note="hypothetical;
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                                                  /transl_table=11
/product="Shf"
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                                       /codon_start=1
                                                                                                                                                                                                                                             /gene="capU"
1403. .2224
/gene="capU"
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/gene="virk"
2453. .3403
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/gene="virk"
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AF326777 66714 bp DNA linear BCT 18-JUN-2002 Shigella flexneri 2a SRL pathogenicity island, complete sequence. AF326777
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             Shigella flexneri 2a
JP94030766-A/1
08-FEB-1994
15-JUL-1992 JP 1992210772
YOSHIKAWA MASANOSUKE
C12P21/21, AGIK39/00, AGIK39/112, AGIK39/112,C12N15/31,
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. (bases 1 to 66714)
Luck,S.N., Turner,S.A., Rajakumar,K., Sakellaris,H. and Adler,B.
Ferric dicitrate transport system (Fec) of Shigella flexneri 2a
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   /product='Shigella virR protein'
Location/Qualifiers
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                                                                                                                   (C12N1/21,C12R1:01), (C12P21/02,C12R1:01);
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0; Mismatches 126;
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/organism="unidentified"
/db_xref="taxon:32644"
311 c 376 g 50
                                                                                                                                                                                        *source: strain=YSH6000T;
*source: clone=pMYSH6000;
                                                                                                                                  strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF326777.2 GI:21450881
                                                                                                                                                topology: Linear;
hypothetical: No;
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Best Local Similarity 65.1%;
Matches 235; Conservative 0
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ECLAVSEHSHVFRQLRYWYOKRTFVAVYSDFWESVAGKTGDWYKLPTGVVRRPLSN
IASKRRSEYRKRYALLDYIHETAIRSLDAYPVNSEHQDLN"
51 a 311 c 376 g 504 t
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                                                                   /organism="Shigella flexneri"
/db_xref="taxon:623"
/plasmid="Plasmid pMYSH6000"
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                                    Location/Qualifiers
                                                                                                                                                                           /codon_start=1
                                                                                                                              /gene="virk"
373. .1323
                                                                                                                                                          /gene="virK"
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E06635.1 GI:2174818
JP 1994030766-A/1.
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Yoshikawa, M.
                            03-3443-3893
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Japan
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/db_xref="GI:15808704"
/translation="MGPAATVDLFNKFVTFTAAQCDQEHIPLIISSIPDIPDRTDALM
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CCLKLFESELYPVCAADAQGHPVFDITQPQVPLLNYTATSYMGRLVNRHLAEVGGITG
RTIFISSMSELLKNWALNGYGTAWLFWSIYDELQTRRLICLDAAKLTVPIQAYIYRM
RTIRTLNRTAENLWRILQEHMPDDLIQQISMEEPARRN"
12299. . 12988
/note="Orf8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKLDKDELEKVLRNIDKFYNAFYSLSVLLDIORTTKILQSLAYYLRVLVREGLMIHGL
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LVFNINDKNGCDDAYLKKIISYFGQLQNEAVHVTSCYETLAVYICLIRKNKINDVLQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MYNANDPNYKMDEWILKDVNEHMDGMFQRFSKLLPFRIDFAYRKD TPSFGHSCKHSMCMEIYRLLSETQTMLAGYYWVMEYTPDKGLHIHFIGYLDGGRHKNS YQISRQLGDIWRRITEGEGYFHLCRAKDKYPYRIDHYTHYSDKSAVDDLRYALSYLAK QDQKEHGILLGRSRLPEKSNRGRPDITELWGLMSELS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSLSRLPFFNKDAYYHLGNYERSDTLRGLITGAWYSALGLELED
HQGLVHFPANGRYILDINDPNFPEQYORLLVRLDYLTKLDTKASGQRNFGYSGF"
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SKYHDPTFPRPIRLGSASVGWRASAIDEWLMLHTAPAWSEPENKLKELNDDDKTITP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLDKINILIDKEYVYDGKTLAEVIMENKVLSSRERKETMIGLFTGSKKYTLLGCVEKL
QVDYIVKSPVESPDEIKNYMMLYGDKAENRNRRMIYDALTIICEDDIRNNPPELS*
7104. . 7697
/note="Orf5"
                                                                                                                                                                                                                                                                                                                                                                                                             CLRTFGVIFLVVDMYNTYRPENDSAFYYHIYNFLQKSYCPCLDHADTESDEAAVKRYL
REYLAELGFNKEDFHENGKLYALGKYTGTIRKDNGKSKSLMQQYIMAIKNEYKKDYRE
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                                                                                                                                                                                                                                                                                                                                                    /translation="MQTNRRAQHMRTFTNMLYDICTVLGLFKEGENPAHKRKSTNFEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDDMERKGLFGELPSGYVRGALSLLRTALEVKVNRKNIKYGSLFYWLDHVKAYQDAFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8449. .8745
/note="Orf6; similar to YfjJ on the cryptic P4 prophage
CP4-57 of Escherichia coli K-12"
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complement(10980. 11918)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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/transl_table=11
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/note="IS629-like element"
10422. .>10905
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QHRVPLSRQAIYILENIRGLHDELVFPSPRKQQILSDMVLTSFLRKKKAVSDIPGRVA
TAHGFRSTFRDWCSEQGYSRDLAERALAHTLKNKVEAAYHRTDLLEQRVPMMQAWADY
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ALDILAEORKIRIDDNLVVYIGNTITPSELAKKINIPAFDAGVFICDHONILKYHRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAVLTDTKARHIKPDDKPLPHGGITGLTLHPSSVKGRGKWVFRY
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IDDKKNYDRUMEMITDKKILERRYKKEIERSPENAAAARAALEKCIANKPEPPYQOV
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                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence updated by submitter
4 (bases 1 to 66714)
Luck, S.N., Turner, S.A. and Rajakumar, K.
Direct Submission
Submitted (18-JUN-2002) Microbiology, Monash University, VIC 3800,
                                                                                                                                                                                                                                                                                                                Luck S.N., Turner, S.A. and Rajakumaı, n.
Direct Submission
Submitted (17-MAY-2002) Microbiology, Monash University, VIC 3800,
                                                                                                                                                                                                                                Submitted (06-DEC-2000) Microbiology, Monash University, VIC 3800,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619. .1836
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/note="member of the P4 bacteriophage integrase family"
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/note="Orf3; similar to AlpA on the cryptic P4 prophage
CP4-57 of Escherichia coli K-12"
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YSH6000 is encoded on a novel pathogenicity island carrying multiple antibiotic resistance genes
Infect. Immun. 69 (10), 6012-6021 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update by submitter
), 2002 this sequence version replaced g1:15808696.
Location/Qualifiers
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    1. .66714
/organism="Shigella flexneri 2a"
/db_xref="taxon:42897"

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/note="SKL pathogenicity island"
519. .1836
                                                                                                                                                                          Luck, S.N., Turner, S.A. and Rajakumar, K. Direct Submission
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BCT 26-MAR-1996

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32345 GATTGCATCGGGCTGAAAACTATGAACTATTCCGAGTAATCTCCATACAGTAGGAATGTG 32404
                                                                                                                                                                                                                                                                         /protein_id="AAA92872.1"
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TLVAVFVAARLIDFIQEGGYAAKGATIISSKNDLIQKKILEEMERGVTILKGQGSYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorokin, A., Rahaim, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 6540)
Sorokin,A.V., Azevedo,V., Zumstein,E., Galleron,N., Ehrlich,S.D.
and Serror,P.
Bacillus subtilis chromosome between spoilA and kdg loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 6540)
Bower, S., Perkins, J., Yocum, R.R., Serror, P., Sorokin, A., Rahaim, Howitt, C.L., Prasad, N., Ehrlich, S.D. and Pero, J.
Cloning and characterization of the Bacillus subtilis bira gene encoding a repressor of the biotin operon
J. Bacteriol. 177 (9), 2572-2575 (1995)
                                          1100 AAGGCTGTTCCTGAAAGGAATAAAAGTGACATCATGCCCTCTTTTTCTGGCTTCCGGAGC
                                                                                                                                                                                                                                                                                                                                                                   L38424.1 GI:755600
biotin [acetyl-CoA carboxylase] ligase; dihydropicolinate
reductase; poly(A) polymerase.
Bacillus subtilis (sub_strain 168, strain Marburg) DNA.
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29. .42
/standard_name="transcription terminator"
/note="putative"
complement(59. .706)
                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                             DNA

    .6540
    /organism="Bacillus subtilis"

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                                                                                                                                                                                                                                                         6540 bp
                                                                                                                                            32465 AATTTTGCTGTTCTCCCTGCAG 32486
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                                                                                                                    1160 AATTTTACTTTTTCTCTGCAG 1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Marburg
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1011. .1346
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AKRELÇPGEWXRNDILAGIFEPATIDIDLAILLTKAREHSVALVGPAAEELFDPVPEQ
DLFEXLNETLTHWNSPPDWAGDXRNVYXTLSXIWXSXYTXKTAPKDYXADWAMERLPA
QYQPVILEARQXYLGGEBDRLASRADQLEEFVHYVKGEITKVVGK*
complement(17075...17905)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAL08435.1"
/db_xref="GI:15808706"
/translation="MREVVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKP
HHGRSPLPVMRDYMHKLEDAGAECTVIPCNTAHYWFKELKDACHIDILSIVETTINEV
RACGKTRICLLATNATLYMGLYQKGIESLGFTCVSPDADGQKKVMESIYSLKAGNIAH
AQKLMNEQAEILFSRGAEILVLGCTEIPVILAQAVKEQPSRYIDSTASLVRAGIKWYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"confers streptomycin and spectinomycin resistance; similar to AadAl from Tn21 on plasmid R100"
                                                                                                                          /transl_table=11
/product="putative anaerobic decarboxylate transporter"
/protein_id="AALO8434.1"
/db_xref="GI:15808705"
                                                            13054...14352
/note="orf9; similar to DcuA in Escherichia coli K-12"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          743 GTCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGTAACGGTCGCATGGCTTCATTATG
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                                                                                                                                                                                                                                                                                                                                                                                       'note="remnant of IS600-like element; central region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="streptomycin adenyltransferase AadAl"
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Pred. No. 4.8e-38;
0; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            complement(15323. .16090)
/note="IS1 element"
complement(16171. .16962)
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                                                                                                                                                                                                                                                                                                                                                                     complement(<14553. .>
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/transl_table=11
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ilarity 58.2%;
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AKEKSLLSHVSVERRTIEFEKLLQGRASRQALQTLIQTRLYEELPGFYHKRENLISTS
ERPPFSLISREELWAALLINGIVLKDAPLFKAWKLPGKVIKEAIHIADTFGQSLDA
WINTRAGKKALLSAAKISQLRQNEKLDEKKLKDIQYAYQNLPIKSLKDLDITGKDLLA
LRNRPAGKWVSEELQWIEQAVVTGKLSNQKKHIEEWLKTCGQH"
5425. .6342
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                                                                                                                                                                          /translation-"mekvfikalpvlrilieachqaypyggayrdsymkriigdvdia
TDAAPDQVERLFQRTVDVGKDESDYVDFRRPSEVQFISSLEEDLKRRDLTINAMAMTA
DGKVLDYFGGKKDIDQKVIRTVGKPEDRFQEDALRMLRAVRFWSQLGFTLSPETEEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="bifunctional biotin operon repressor"
/note="26.7% identity to the Escherichia coli bifunctional
biotin operon repressor"
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1 (bases 1 to 10801)

Yocum, R.R., Patterson, T.A., Hermann, T. and Pero, J.G.
Methods and microorganisms for production of panto-compounds
Patent: WO 0121772-A 76 29-MAR-2001;
OMNIGENE BIOPRODUCTS, INC. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="blotin [acetyl-CoA carboxylase] ligase"
/protein_id="AAA92879.1"
/db_xref="GI:755608"
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Pred. No. 9.9e-09;
0; Mismatches 108;
                                                                    /product="polyA polymerase"
/protein_id="AAA92878.1"
/db_xref="GI:755607"
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Sequence 76 from Patent WO0121772.
AX100832
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/gene="bira"
5425.
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/gene="birA"
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3229. 4302
3229. 4302
7gene="jojH"
7note="1.6% of identity to trans-acting transcription factor of Sacharomyces cerevisiae; 25% identity to sucrose farther of Sacharomyces, putative"
7codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MSNETIKLVIAGPRGRMGGEAVKLAERTPHFDLVGAIDHTVDQQ
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LDAPSGTALKTAEMISEVRKEKQOGHPDEKEILPGARGAEQNGIRLHRAOIRNDSYNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="managere.1"
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IPLATNMGTAEILVRTLDEGVFEFRDLLRGEEPNV"
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                                                                                                                                                                                                   /function="1ysine biosynthesis"
/note="28.2% of identical aminoacids with the Escherichia
coli dihydropicolinate reductase; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4307. :5440
/gene="paps"
/note="38.9% of identical aminoacids with the Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli pcnB gene product, encoding poly(A) polymerase;
                                                                                                                                                                                                                                                                                                                                                                             /product="dihydropicolinate reductase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASFMSGVKLSVEQVMKIDQLVYGLENIID'
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2117. .2530
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                                                                                                                                                                                                                                                                                                                                                       /transl_table-11
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/note="putative"
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1358. .2101
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                                                                                                                                                                                                                                                                                                                                                                                            EWGDVERAISLISDLHULYPRITELLINEYAELLIDIDEBERALAVLETIPETDESTER
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ALPLIKKYLEMDGANEELEETILRIEDFESA
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/note="26.2% of identical aminoacids with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Rieske iron-sulfur protein"
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2 (bases 1 to 23775)
Sorokin,A., Azevedo,V., Zumstein,E., Galleron,N., Ehrlich,S.D. and
                                                                                                                                                                                                                                                                                                                                                             335 GCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAAT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 AGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACCACTGGCAATCCG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACYPIA 11near BCT 09-AUG-200 Bacillus subtilis (clone YAC15-6B) ypiaBF genes, qcrABC genes, ypjaBCDEFGHI genes, bira gene, panBCD genes, dinG gene, ypmB gene, aspB gene, danB gene, nth gene and ypoc gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 GTAGACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGCTCATTCC 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Mugh_ _____/Clone="YAC15-6B"
/clone_lib="chromosome YAC library of Pascale Serror"
/clone_lib=acas 57126 to 80902 of the YAC15-6B clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial
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                                                                                                                                                                                                                            Length 10801;
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/citation=[2]
                                                                                                                                                                                                                                                                                             0; Mismatches 108; Indels
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2485 c 2151 g 3368 t
                                                                                                                                                                                                                                DB 6;
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96349105
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Pred. No. 1.1e-08;
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                                                                                                                                                                                                                            Query Match 5.4%;
Best Local Similarity 54.4%;
Matches 129; Conservative
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L47709.1 GI:1146223
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Bacillus subtilis
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Bacillus subtilis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

I (bases I to 213680)

Kunst, F., Ogasawara, M., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borniss, R., Burschi, C. V., Caldwell, B., Caphanno, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S.C., Broni, J. J., Connerton, I. F., Cummings, N.J., Carter, N.M., Choi, S.K., Codeni, J. J., Connerton, I. F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Guy, B.J., Haga, K., Haiceh, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Klain, C., Kobysshi, Y., Koetter, P., Khain, C., Koogh, S., Kumano, M., Kurita, K., Levine, A., Liu, H., Masuda, S., Mauel, C., Medique, C., Median, N., Menerlo, M., Medique, C., Medina, N., Menerlo, C., Medique, C., Medina, N., Moore, D., O'Reilly, M. Ogawa, K., Ogawa, R., Oudega, B., Perscott, A.M., Parro, V., Pohl, T.M., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Sakiguch, J., Schletch, S., Schroeter, R., Scoffone, F., Sakiguch, J., Schols, B., Raconi, E., Tarkamaru, R., Tarakoshi, H., Tarkamaru, Tarakoshi, M., Tanaka, T., Taraka, T., Tarakashi, H., Tarkamaru, Taskana, L., Wedler, F., Wedler, H., Weitzenegger, T., Varain, A., Wannutt, R., Wedler, F., Wedler, H., Weitzenegger, T., Winters, P., Wilpat, A., Yamanoto, K., Yamanoto
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Bacillus subtilis complete genome (section 12 of 21): from 2195541
to 2409220.
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DWAKAEEQGKITKEADIDTNAEGYKVFKEQGCISCHGDNLQGGAAGPSLVDSGLKPDE
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LRAAAQFRMLMDAVDNRSDPLWGSLEKPIMEAFTELKRDVQKNGSTSFHEKWNEFISL
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EEDDADPSLLWVIITTGSIIITALTYVGYRKYKAERNKLKKRDYPK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="29.1% of identical aminoacids with the Spinacia
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5628. .6422
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4088. .4855
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                                                                     complement(2014. .2466)
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                                                /gene-TyogH
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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Buret Submission
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,

Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724

Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,

68.89 48
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LKIKNYRLORDAHKKHNITDVOWOKCKDYFNNKCSYCGIKIEDHKILFKGTYIOSDFH
KEHVDHKGANDISNCIPACKSCNSSKHDFAFEEMYNSSNKNFSSERLIKIKEWINRFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="similar to hypothetical proteins from B. subtilis"
                                         The complete genome sequence of the gram-positive bacterium
Yoshida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                            /organism="Bacillus subtilis"
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Nature 390 (6657), 249-256 (1997)
98044033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="yoqL"
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                                                                                                                                                                                                                                                                                                                                                                                                 /strain="168"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="yogk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALUNS927 13-JUN-2001 Xylella fastidiosa 9a5c, section 73 of 229 of the complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394
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Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M.,
Simpson, A.J.G., Reinach, F.C., Araya, J.E., Baia, G.S., Baptista, C.S.,
Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S.
Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M.,
Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 AGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCG 514
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Pred. No. 2.1e-08;
0; Mismatches 108; Indels
                                                                                                                                                        LVLSKRFRNPEDPNKYRYLRSVEEFFESYAAKK"
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Nature 406 (6792), 151-157 (2000)
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Xylella fastidiosa 9a5c
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Costa-Neto,C.M., Coutinho,L.L., Cristofani,M., Dias-Neto,E.,
Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S.,
Forreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,M.C.,
Frohme,M., Furlan,L.R., Garnier,M., Goldman,G.H., Goldman,M.H.S.,
Gomes,S.L., Gruber,A.H. Bo,P.L., Hohelsel,J.D., Junqueira,M.L.,
Kemper,B.L., Kitalima,J.P., Krieger,J.E., Kuramac,E.E., Lalgret,F.,
Lambais,M.R., Lelte,L.C.C., Lemos,R.G.M., Madcira,A.M.B.N.,
Madcira,H.M.F., Marino,C.L., Marques,M.V., Martins,E.A.L.,
Mattins,E.M.F., Marsiuma,A.Y., Manckor, E.C.,
Mayaki,C.Y., Monteiro,Willo,C.B., Moon,D.H., Nagai,M.A.,
Nascimento,A.L.T.O., Netto,L.E.S., Nhani Jr.,A., Nobrega,F.G.,
Nunes,L.R., Oliveira,M.A., de Oliveira,M.C., de Oliveira,M.A.,
Palmieri,D.A., Paris,A., Perxoto,B.R., Pereira,G.A.G., Pereira
Jr.,H.A., Pesquero,J.B., Quaggio,R.B., Roberto,P.G., Rodrigues,V.,
Gawasaki,H.E., da Silva,A.C., G. Santelli,R.V.,
Sawasaki,H.E., da Silva,A.C., G. Silva,F.R., da Silva,A.M.,
Tsuhako,M.H., Vallada,H., Van Sluys,M.A., Verfovst,A.Lmeida,S.,
Direct Submission,
Direct Submission,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="outer membrane protein"
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GLDQNRRLDPMSVGFGIGRRF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"outer membrane protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLAKGGIQLDIRVENDYVQPNDQVAQKQIDVNYFQTEPYLQAYNRSRNTHLITVVGVH
IEPFGAYSRRYTALASLPKGAEIAIPNDPSNNSRALIILHQAGLIKLKDPKNMLATQR
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NYLVSREDNKDDPRVQKLAKALTSPEVKDFIDKKYGSAILPAF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SP|P21364 (percent identity: 30 %/query alignment coverage: 87.3 %/subject alignment coverage: 74.5 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-2000) organization for Nucleotide Sequencing a
Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xylella fastidiosa 9a5c"
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/clone="9a5c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1626. .2333)
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/gene="XF0873"
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/gene="XF0873"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
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96. .641
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CDS

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5398. .6510
/gene="XF0879"
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95.4 %); identified by sequence similarity; putative; ORF
located using Glimmer/RBSfinder"
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DALRPDPRVRRAMLHELGWDEDVLVVGCFGRIEGGRGYFVLARAMEQBMQGEFRLCCT
WMGTGLHVQRLAATVAGSRFASRQRVLGWVTDPARXFQALAMIAMPSLLPEFFGRRVSA
AHGFSATCYVVSGSLARFNTWDAERLNVCKPLMSPAQVRQWHDAGMEVCAHTRSHPHL
SGCTAAQLHEEIAGCRDDLEQCIGAPVTQFCYPYGDVTPPVIDAVCDAGYAAATTTRR
GRVFPGQHLWTLPRVPVSYRHILPQPALRTLTGYEDRRI"
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1 (bases 1 to 1424)
Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
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Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6395 GCTGCTGCCATCGCGGGCTCGCGGATCACAAAATGCCAGAATCGCATTCCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 GCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGG
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Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 13334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59.2; DB 1;
Pred. No. 4.9e-07;
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Mycobacterium tuberculosis CDC1551,
                                                                                        /gene-"XF0879"
5398. .6510
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Best Local S
Matches 130
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                                                                              gene
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AE007070
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AUTHORS
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KEYWORDS
SOURCE
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                                    //octe="similar to GI|2635771 (percent identity: 48 %/query alignment coverage: 95.2 %/subject alignment coverage: 93.3 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder/Start codon shift: 30" /codon_start=1
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LLCDEVTSALDPQTTTAQLLARINRELGITIVLITHEMDVIRRICDRVAULDTGRL
VETGLYTDVFLHPQHPTVLSYPWETBHIDTSALDQDFSLVNGRIVRLFIGTDYTLPL
LGRVARETGVDYNILSGRIDRIKETPYGQLTVALSGGDPVAAQAAFAAAGIHIEELRA
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/Agene="XxP0877"

/note="hypothetical protein; identified by sequence

similarity; putative; ORF located using Glimmer/RBSfinder"

/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Lanslation-Meltalfrosnhdvyaviahcsayrarciahftgsyggpelhie
Ivlimarqrsaqhnavcriporiehtdqqrealavqgsyrqyrreserrnqriclidy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /LTAINSLATION="MLGVLCRRRRFTCGHQTFGQFVQRGCLLFQMGEESRWQVVHIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GII1783247 (percent identity: 29 %/query alignment coverage: 84.4 %/subject alignment coverage: 77.8 %): identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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complement(3752..4060)
/gene="XF0876"
                                                                                                                                                                                                                   QLIQMFGDWLVAHYSRR"
complement(2330. .3334)
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                       /transl_table=11
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4321. /fc2
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/gene="XF0878"
4628. .5401
/gene="XF0878"
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CDS

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ARRWDRIVVDCASTADALRMLTLPATFGLYVERAWPRHRRLSIGADDGRSAVLAELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AaK46524.i"
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GGGGTGASGGENTNGEGSMKSHYQAIPVTIEE"
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VODENTEYRELDHPREMYAERIGEORAVLDDLARIGDVALVLVPHLAGEPIGPKA
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LIVSAGGMRRRVRLASVLRRCTVLDAHLRGGELTVRFRPNPEWPPT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MWYYLEKYIFWGPLFTLLGRPRVEGLEYIPSSGPAILASNHLAV
ADSFYLPLVVRRRTWFLAKSEYFTGFGLKGWITNRWFYSVSGQVPIDFTNADSAQGALQ
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GRKMLRFGRYVVRFGRPMDFSRFEGLAGNHFIERAVTDEVIYELMGLSGQEYVDIYAA
SVKDGRNAGGAGANNSTDAARIPETAAG"
complement(6235..6639)
                               SVDGREPEFTIAASIFGVGAALVLDEYALILHLSDVYWEEDGRTSVDAVFAAVAVAGL
LIUGLHPLIFERLPWRQGANWVYLQTTLIAGLVTLTPLAVVULKGKVWFGLLGMEVVY
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SNFABGQINVYLMTIVIVDCEPRRTPWFRGLWLGLGIALKTPAVFLLYFLLKRDGRA
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LPAVLYIGLLGWRRRNYALAMLSLAGVYLMRWPPIDLLPQHRETTAVWWRQLAGMSYY
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polmhercarrelasipsigredgasarviselgadpamwrsesaehlaswyrlognu
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aliavahkliviiwhvlatgrpygolgadysttremdpdkerrrlvakleagglgytle
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Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W. Direct Submission.
Direct Submission.
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:AL123456; identified by sequence similarity; putative"
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                                                                                                                                                                                                          /organism-"Mycobacterium tuberculosis CDC1551"
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complement(2631. .3137)
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complement(3147. .4085)
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                                                                                                                                                                                                                                                                                                           /note="clinical strain" complement(102. .767)
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CDS

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available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes inplemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CATION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, 9tg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                               tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 20, 1998 this sequence version replaced gi:2911087.
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BUVGRREGPAPNRIWWADLITVSTWAGFAVYAPTVDAYARAILGWRASTMATSMV
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NALAETINGLYRTELLIKPGRPWRSIEDVELATARWVDWFNHRRLYQYGGDVPPVELEA
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                                                                                                                                                                 2 (bases 1 to 23400)
Parkhll,J.
Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of M. tuberculosis sequencing at the Sanger Centre are
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/note="fragment designated v021. Does not represent a
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/strain="H37Rv"
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/note="ISS110 insertion element"
complement(115. .142)
/note="Inverted repeat at end of ISS110;
complement(15. .1197)
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                                                    complete genome sequence
Nature 393 (6685), 537-544 (1998)
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/ftanslation="MADKTYOTYIDADPGEVMKAIADIEAYPQWISBYKEVEILEAD
/ftanslation="MADKTYOTYIDADPGEVMKAIADIEAYPQWISBYKEVEILEAD
/GTSYRKARMLMDATFKDPLIMSYEWPEDROSLSWTLESSSLLKSLEGTYRLAPKGS
GTEVTYELAVDLAVPWIGMLKRKAERRLIDGALKDLKKRVEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mnsiqiadetyvaadaarvsaavadrcswrrwwpdlrlqvytedr
ADKGIRWTVTGALTGTWEIWLEPSWDGVLLHYFLHAEPTGVAAWQLARMNLARWTHHR
RVAGKKMAFEVKTVLERSRPIGVSPVT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391
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Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Tekala, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,
Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 AATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis H37Rv complete genome; segment 97/162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTCTGGCGCTGCCTCCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 TGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GP:4539200; identified by sequence similarity; putative" /codon_start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 14243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 23400)
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
/protein_id="AAK46527.1"
/db_xref="G1:13881930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8%; Score 57.2; DB 1; Length 1.
4.2%; Pred. No. 2.2e-06;
ve 0: Mismatches 98; Indels
                                                                              hypothetical protein"
                                                                                                                                                                                                                                                                                                                                /gene="MT2241"
/note="identified by Glimmer2; putative"
/codon_start=1
/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11074 Trccaggaacaccarcccaacccrccaccrcc 11107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 ITCAGCCAGTACCATACCAAACGCTTCATTTTCC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis H37Rv. Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                  complement(8425. .8814)
/gene="MT2241"
                                                                                /product="conserved hyp
/protein_id="AAK46526.1
                                                                                                                                                                                                                                                                                                      complement(8425. .8814)
                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8971. .10782
/gene="MT2242"
8971. .10782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8971. .10782
/gene="MT2242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL021957.1 GI:3242293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1larity 54.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272
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SOURCE
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20131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTLNTIALELVPPNLEGGKERALEDARKVVQYSAASGLDGRIRH
VMMPGMIAEDDDRPIPWQPKLDVLDFWSIIKPELAGVHGLCTQVTAFWDEPSLHRRLV
DLSDAGMEGIVFVGVPRTMQDGEGSGVAPTDALSLYRQLVANRGVIVIPTRDGEQGRL
                                                                         /translation="MARTRREGMLAIAMLAMLWPLATGCLRVRASITISPDDLVSGEI
TAAAKRUSKOTGPALLGGDVPESQKVANNIDDEDGYVGSQAVEBULFRELPQCLANNN
SDAAGVVLSLRRNGHYVILEGRADITSVSPDADVELTVAFPAAYGYNGDRIEPEVY
OWKLKPGVVSTWSAQARYTDPNTRSFTGAGIWLGIAAFAAAAGVVAVLAWIDRDRSPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQDPGNAAVADEQAFVQKLAGSEPARRRIAWVDLYKRVLDGVADLGFPLSIHLEATYG
VSAAAFETFAEMLAYWSPAEPGKPD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391
                                                                                                                                                                                                                                                                                                                                                                                                             complement(3529. .4534)
/gene="Rv2172c"
/note="Rv2172c, (MTV021.05c), len: 301. Unknown. TBparse
score io.905"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 TTCTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 TGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 AATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGC
                                                                                                                                                                                       2991. .3023
/genem="lppM"
//note="PS00013 Prokaryotic membrane lipoprotein lipid
attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                 key,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 14734)
Raymond, C.K., Sims, E.H., Kas, A., Spencer, D.H., Kutyavin, T.V.,
Ivey, R.G., Zhou, Y., Kaul, R., Clendenning, J.B. and Olson, M.V.
Genetic variation at the O-antigen biosynthetic locus in
                                                                                                                                                                                                                                                                                                                            Crystallins beta and gamma 'Greek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 23400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein Rv2172c"
/protein_id="Caa17476.1"
/db_xref="G1:2911092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20252 TTCGAGGAACACGATGCCCAAGCCCTCGACGTCC 20285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57.2; DB 1;
Pred. No. 2.5e-06;
0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 TTCAGCCAGTACCATACCAAACGCTTCATTTTCC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:053506"
                                                    /db_xref="SPTREMBL:053505"
    /protein_id="CAA17475.1"
/db_xref="G1:2911091"
                                                                                                                                                                                                                                                                                                                                                                          complement(3629. .4534)
/gene="Rv2172c"
                                                                                                                                                                                                                                                                             3162. 3209
/gene="lppM"
/note="PS00225 Cry
motif signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:20560066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.8%;
                                                                                                                                                                    TASGDPPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.23
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas.
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                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                              misc_feature
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KEYWORDS
SOURCE
ORGANISM
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AF498417/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                    transposase FASTA scores: sptr|008155|008155 HYPOTHETICAL 12.0 ND PROTEIN (108 aa) opt: 697 z-score: 903.5 E(): 0; 100.0% identity in 108 aa overlap. TBparse score is 0.928" /codon_start=1 /frans_table=11 /prodince=10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ipoproteincontainsputative signal peptide and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachmentsite. Has hydrophobic stretch att C-terminus and also contains PS00225 Crystallins beta and gamma 'Greek key' motif signature. Unknown but similar to TBparse score is 0.895"
                                                                                                                                                                                                                                                                                                       /db_xref="SWISS-PROT:Q50686"
/translation="mSGGSSRRYPPELRERAVRWVAEIRGQHDSEWAAISEVARLLGV
GCAETVRKWVRQAQVDAGARPGTTTEESAELKRLRRDNAELRRANAILKTASAFFAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:053503"
/translation="MPLSPHERMLDOIESALYAEDPKFASSVRGGGFRAPTARRRLQ
/translation="MPLSPHERMLDOIESALYAEDPKFASSVRGGGFRAPTARRLQ
AAALFIIGIGALVSVAFKEFMIGSFPILSYRGFVVMFGGVYYAITGFRLSGRWDRGG
SAAGASRQRRTKGAGGSFISRMEDRFRRRFDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:053504"
/translation="MAIFLIDLPPSDMERRLGDALTVYVDAMRYPRGTETLRAPWWLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIRRRGWOAVAAVEVTAAEGAEAADTTALPSAAELSNAPMLGYAYGYPCAPGGWWQQQ
VVLGLQRSGFPRLAIARLMTSYFELTELHILPRAQGRGLGEALARRLLAGRDEDNVLL
STPETNGEDNRAWRLYRRLGFTDIIRGYFFAGDPRAFAILGRTLPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1563...1967)
/gene="Rv2169c"
/note="Rv2169c, (MTV021.02c), len: 134. Unknown. TBparse
score is 0.934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2233 . 2853
/gene="Rv2170"
/note="Rv2170, (MTV021.03), len: 206. Unknown. TBparse
score is 0.905"
                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv2168c"
/note="DRA1:TTTAAA. Site linking fragments L-T"
/note="DRA1:TTTAAA. Site linking fragments L-T"
/note="INATA repeat at 5'-end of 186110"
complement(1553. 1967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2949. 3632

2949. 3632

2949. 3632

//note="TppM"

/note="Rv2171, (MTV021.04), len: 227. Probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1973. 1979)
/note="possible RBS, aaggagg, for Rv2169c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        938. .2942
note="possible RBS, aggagga, for Rv2171"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="possible RBS, aggagga, for Rv2170"
                                                                                                                                                                                                                                    /product="hypothetical protein Rv2168c"
/protein_id="Caal7472.1"
/db_xref="GI:2911088"
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/protein_id="CAA17473.1"
/db_xref="G1:2911089"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein Rv2170"
/protein_id="CAA17474.1"
/db_xref="G1:2911090"
complement(1092. .1418)
/gene="Rv2168c"
complement(1092. .1418)
/gene="Rv2168c"
/fote="Rv2168c"
                                                                                                                                                                                                                                                                                                                                                                                                  complement(1141. .1146)
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/codon_start=1
/transl_table=11
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INELAIIFNRMGIDTEAVLKAAGTKWNFMPPRPGLVGGHCIGVDPYYLTHKAQSIGYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roffrdvy ipsleegasvgsrdolyallmnsvy iokpskedsery tvv ierhdpsqaa
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ALRARALKENPPLIEGQVDQQLSSIMEGGLMYMRGAKAIRAETKTLQDRVSDDPFIP
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AENIRKLGKAEHVLYDLKYLLDEDKSDLRL"
3670. 4695
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                                                                                                                                                                                                         Center, University of Washington,
1145, USA
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/note="ORF_4; wzz; similar to chain length determinant
                                                                                              Chases 1 to 14734)
Raymond, C.K., Sims, E.H., Kas, A., Spencer, D.H., Kutyavin, T.V., Ivey, R.G., Zhou, Y., Kaul, R., Clendinning, J.B. and Olson, M.V. Direct Submission
Submitted (04-APR-2002) Genome Center, University of Washingto Box 352145, Seattle, WA 98105-2145, USA
On May 13, 2002 this sequence version replaced gi:17975265.
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                                                                                                                                                                                                                                                                                                             1. .14734
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Pseudomonas aeruginosa
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                                             MEDLINE
PUBMED
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ETRYPLIDHRVFELAWRMPLHMKIRNGKGKMLLREVLYRHVSRELIERPKKGFSVPVS
DWLRGPLKEWAESLLDERRLQQEGYLDSRLIRRIWNDHLAGRRDHSRRLWSVLMFQAW
                                                                                                                                                                                                                                                                                                                                                    SVPRSINDPITSNATNIDGFLNMLIAARDAKVQSFTYAASSSTYGDHPGLPKVEDTIG
KPLSPYAVTKYVNELYADVFSRCYGFSTIGLRYFNVFGRRQDPNGAYAAVIPKWTSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                 IQGDDVY INGDGETSRDFCY IENTVQANLLAATAGLDARNQVYNIAVGGRTSLNQLFF
ALRDGLAENGVSYHREPVYRDFREGDVRHSLAD ISKAAKLLGYAPKYDVSAGVALAMP
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GGSDTETLLACFAQWGVESTLKLIVGWFALALWDRQEKTITLARDRMGEKPLYWGWQN
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                                                                                                                                                                                                                                                                       /translation="mmSryEELrkELPaQPkvwLtTGVaGFIGSNLLETLLkLDQRvv
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DHIVCGNQYLADYFGQFGRPTTIIPTGVDTLRFLPRRERRENRYIGWSGTSGGYRFLY
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/note="ORF_6; similar to NAD dependent
epimerase/dehydratase family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYLAAMIALDVSGMRTFLKSKLIR"
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                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 16736)
Belanger, M. and Lam, J.S.
Direct Submission
Submitted (26-NOV-1997) Microbiology, University of Guelph, Guelph, Ont NIG 2W1, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"XPKLEEGVEGLVHVSEMDWTNKNIHPSKVVQVGDEVEVQVLDID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDIAGFNLGRSENGLPAFSANGVYSIFVRNLQSEETRRQFFRDVYIPSLEEGASVGSR
DOLYALLMUNSVYIQKBKERDSBRYYVYIRTBHDPSQAARWGERYIGIAVKRSMQERQUEG
VRREPQVKRNNIQQDIDILERTAKARREDRISRLKEALRVARAKSKLENPPLIEGQVDQ
OLSSIMEGGLMYMRGAKAIRAEIKTLQDRVSDDPFIPALRGLQEKYALLEGLITALDLA
                                                                                                                     Pseudomonas.

1 (bases 1 to 16736)

1 selanger, M., Burrows, L.L. and Lam, J.S.

Functional analysis of genes responsible for the synthesis of the B-band O antigen of Pseudomonas aeruginosa serotype 06

1 ipopolysaccharide
                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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/organism="Pseudomonas aeruginosa"
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                                              Pseudomonas aeruginosa.
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                                                                         Pseudomonas aeruginosa
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1954. .2811
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  AF035937.1
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                                                                      ORGANISM
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TITLE
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MEDLINE
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AUTHORS
TITLE
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Digregoglieagisydvlghtsmedmprvlirlimifrerrpdivqtwmxhsdligg
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Augynalarlvipurgelltrigatdegasairsgagieasdivigslgrehpvkdhas
FVAAAGLERRYSRFLVGRELLSSNAELQRIIBATGYARRFILLGERQDVASCLK
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RLAPVKGVVAAVSGLGFVFMAKGLRACAFRACVAMLYRRALGKKKLRVIFQNPDDRDA
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LPSYREGIPRVLVEASACGRAVVTTDVPGCRDAIQADVTGLLVPVRDSAALADAIQRL
IESPELRKKWGAAGRALAERDFAIESIVQQHLDIYRALGSGA"
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SAGALLDLABETGLEVVIIRPVLVYGPGVKANVOTMRRNLKRCVPLPLEGAIHNRNSLV
SLDNLVDLIITCIERAAVGOPTKSUGGELSTTELLRRMGRALGAPARLLPVPASWI
GAAAKVLNRQAFARRLCGSLQVDIMKTRQVLGWTPPVGVDQALBKTARSFLDRQ"
                                                                                                                                                                                                                                                                                                                                                                                                      LIGLGAITFEKSVLIRGSGVDLTQYQPAPESPETPVVTLAARLLRDKGVLEFVEAANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'translation="MLLGELGSSVVWDAESAIDTVVHCAARVHVMSETASDPLVEFRK
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/note="ORF_12; similar to Glycosyl transferases group 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group 4;
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potential multiple membrane spanning domains."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11839. .12657
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epimerase/dehydratase family"
                                                                                                                                                                                                                                                           /transl_table=11
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Matches 14
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AF035937/c
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12355 TGGACGATACTTTCGATCGCAAAATCACGCTCTGCCAACGCTCGCCCAGCAGCTCCCATC 12296
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                                                                                       RAPILVHARLAVLELSPAGSQPMHSDCGRYVLIYNGEIYNHLALRARLSEAGYTHSWR
GCSDTETLLACFAQWGVESTLKLTVGHFALALWDRQEKTITLARDRWGEKPLYWGWQN
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NSKDALDVIPSLPKIYCEPFGDSSQIPTLIVSGLARQOYTVALSGDGGDELFGGYNPY
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11268 . 12398
4900="Whydu"
11268 . 12398
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ETRYPLIDIRVFELAWRMPLHWR TRNGKGKWLLREVLYRHYSRELIERPKGFSVPVS
DWLRGPLKEWAESLLDERRLQQEGYLDSRLIRRIWNDHLAGRRDHSRRLWSVLMFQAW
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LAARWAGIGGIIWGVRTTDLQEGGKSTTVLVRKVCAWLSGFLPRYIVCAAEASRRSHI
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Pred. No. 2.7e-06;
0; Mismatches 145; Indels
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10073. .11224
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ALRDGLAENGVSYHREPVYRDFREGDVRHSLADISKAAKLLGYAPKYDVSAGVALAMP
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ERVEFIRWTETNEVETIAGNDIGIMPLADDIMSRGKCSYKMLIYMACGLPVVSEYGM
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                                   INELAIIFNRMGIDTEAVLKAAGTKWNFMPFPGLVGGCTGVDPYTLTHKAQSIGYH
PEIILAGRRLNDGMGAYVSQLVKAALKRRIHYDGARVLLMGLTFRRNCPDLRNTKVV
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RAPCQRALOGYUDEFGKLÚLÍ LNNAAČDHOGES I EDÍTKEGUERTEKTNÍ SMETLÍTK
RAIKHLKKGSAI INTTSVTAYKOSPOLLDY SSTKGATVAFT RSLSGNILSKGIRVNAV
APGPIWTPLIPSTFPAEKVETFGKOVPMQRAGQPEEVAPSY VFLASDDSSYMSGQVLA
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KENMTIGGALERIRSLANASEMIYYLYVTDQARRLTGIVSLRELVTSQPEQTIGEVMT
RDVIFVNTDTHQEEVARLIQRYDFLAVPVVDRQQLLVGIVTVDDVIDILEEETTRDIY
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WAYFLQGRIEVAIAVGASLIAISVLASISGSALPFLFRYLRLDPALASAPFITTAVDV
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VAHVGLYESQDVETIKIPFSSVDRAIADGQEDGFLKIHHKKGSDBIVGATIVASHAGE
MISEVTTAIVNKIGLNKLSNVIHPYPTQAEAIKKAADTYRRTLLTPRTKKLLGFLTKF
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PVOPADIAEAIEGLPETMHALAFRLLSKDEAIEVYEYLDYSVQERLIEELKSQEVRDI
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KNLGVNIPSQIDIDFPAVMARMRRVRAGISHNDSAERFASLGVDVFLGSGRFASSNTV
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complement(5361. .6890)
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                                                                   APU03599 237221 bp DNA linear BCT 28-NOV-2001
NOSTCC SP. PCC 7120 DNA, complete genome, section 19/19.
AP003599 BA000019
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RYWOKAGYDHKIDLYLAPALETLDKILLVAGEAETFDFAFIDADKSNYDNYERSLOLI
RSGGVIAIDNYLWSGKVADPEIQDNRTQKIRAFNHKILLQDQRITLSLIPIGDGLTLVR
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SHPLARERFITDGYDLFIERYGSLINASKSYKTELKDAFNAHLERIEPDDTGLAIKLY
PFTRSHEEDNPRFVVVDPRIAFGRLVIVGTGISTRVLAERYQAGESIDELAYDYDCDR
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                                                                                                                                                                                                                                                                                                                          Kaneko,T., Nakamura,Y., Wolk,C.P., Kuritz,T., Sasamoto,S.,
Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K., Kimura,T.,
Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Muraki,A.,
Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yamada,M.,
Yasuda,M. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:Kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp,
Tel:81-438-52-3935[ex.2338], Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120 DNA Res. 8 (5), 205-213 (2001)
                                                                                                                                                                                                                                                                               Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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/gene="alr5180"
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                                     RESULT 25
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74410 AATATCAGGGCCTGCTGTATTATAAGTTGTAATTACAGGAATTCCACAAGACATGGCTTC 74351
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ALAAALGTILSDPALAQRLGQSGREDVSDRFSLQETCRSVSALLTEAA"
1396. .2514
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DPFGSPLGGKRRLTLVHDLYFKTIPEQIGWRATLTTDFIFRLMMAGSNRVVCVSEATR
KDLARFYPAAATKSLTIHSDSTLSVDPDPVDTASPIAGRYILAVGNATSNKNFALLGK
                                                                                                                                                                                                                                                                                       BCT 18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 10197)
Hinkle,G., Slater,S.C. and Goodner,B.
Direct Submission
Submitted (14-AUG-2001) Bioinformatics, Cereon Genomics, 45 Sidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1396 . . . . . . . . . . . . . . . /gene="AGR_L_2543"
/gene="mannosyltransferase B - Synechocystis sp. (strain
                                                                                                                                                                                                                                                                                  10197 bp DNA linear BCT 18-DEC-200
ons str. C58 linear chromosome, section 131
                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens str. CS8 (Cereon)
Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group;
Rhizoblaceae; Rhizobium.
1 (Dases 1 to 10197)
Hinkle,G., Slater,S.C. and Goodner,B.
(Complete Genome Sequence of Agrobacterium tumefaciens CS8
(Rhizobium radiobacter CS8), the Causative Agent of Crown Gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the left
                                           455 AGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Street, Cambridge, MA 02139, USA
Approximately 800 bp of telomeric sequence missing from the
end of the chromosome and 200 bp missing from the right end.
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/gene="AGR_L_2541"
219. .1367
/gene="AGR_L_2541"
/note="(Y17900) putative hexose transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens str. C58 (Cereon).
                                                                                                                                                     74290 GTAATACTGGTTCAGAAGTAAATGGGGAACTGAC 74257
                                                                                                                          515 GTAGACCGGTAACGCTGGGAAAAGGGCACCTGCC 548
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/protein_id="AAK89839.1"
                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens str. Coof 187 of the complete sequence. AE008327 AE007870
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LAETFFRHPGQVLSRRQLLDRVWGYDYDFGSNIVDVYVGYLRKRLGNDLIETVRGMGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="two-component sensor histidine kinase"
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YKSSPRARFRENDRAKLIRDWAKLTQPRQERVIPSNGVDSIVYLARPVETGEIMG
STRIATAGERGEVLETLAVIVQVSTFVLIFALVALAMLASGKILAPLRLITGTARK
SETDLANGRITTDGNGELALGYTRUNAMDRLONAFISGNRFTNDAGHELRFPTTIIRG
HLELMGNDFKEIQETLITVIDELERNNFVNDLALLARAERPDFLLLEFFDVCTFTEE
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                                                                                                                        /transl_table=11
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                                                                                                                                                                                                              VQSLGFFGPIAYMIIYNLATLLFIPGSILTLKSGCLFGVFWGSVTVLIAATVGAILAF
EIGRYLSRUWVRQIDKYPREKMIDQSVAKEGWKIVLLTRLSPVFPFWILNYAFGYTC
ISLKDYILGSLGII FGTIMYVYIGSLAGDIALAGTNHQPVTPETQIWQWINGGLGLAA
TYGVTVYIIKIAQKALSQKVVTEGIIKSQDAE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 GCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAAT
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Pred. No. 2.5e-05;
0; Mismatches 137; Indels
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7989. .8657
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                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF_ID:asr5187
                                                                                                                                                                                                                                                                                     /ooy. .8011
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7859. RA11
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                                      /gene="alr5186"
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RSAFLLRFFRIVPLYWFTTANAAVPTIIGAKAFPPEWSNLVYLVISTVAIA
HAFHVFVFTFANMINDRLITSKAVS"
1 2826 c 3116 g 2075 t
                                                                                                   DVLLRDEKTYLAFLPTVVKQRVPHSSELLTSAOMHKLLAEASSAFDYIIVDLPPLGFV
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complement(8453. 9445)
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PSEGKSTISINLAQLLAGGGARVLLLDADIRNPGATRAMARHAAEGLLEVLLEGRSVQ
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          ASETQVQMRELQREAETYKNMYQTFLQRYQEAMQQQSFPVTEARVISKAMPPYMPSKP
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                                                                                                                                                                                                                                                                               /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="AGR_L_2557"
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Irliadldangadpasasgmarvdfaetfirhsleclpangdwirlamyrsliras
Pmevavlamysglyfspadamiirgervwworfgrdebardadyvckegeei
Irwtlaavcprppesgtkrpatlp"
                                                                                                                                                                                                                                                                                                                                                                                                  DGHICDGSSKKCRAFSYLHRRCQCSVDAVAGVGRDIVERHVRAGFFTHVPESRRTVIW
NAISPPDARRCTARAPGARVAPLVRGYLGRIEAAKGADLLIEALRFLPSQGWRLVWA
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VPVIGANLAGVAEOIGFEROERLEFAGNAAELAARWAEAMRNPAMLTETPETRERIRG
GVAPEVVVAAYEKLYSDVRSSTQP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRSLSDRLLNDLSVKRIGRTYALELTYNSTSPVLAAQIVNAVASAYLLDKLNSKYEAT
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AAQTLRWFAIAGGWLALFSIVQFALFPDALGFIQKRFYLGSLTGLFVNRNTAATFFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILLTLATLLHKSLLAPDWAWVKALVANRLTVPADQKKLIRKSVFIGVLAGFSFTALML
TGSRAGIASSLAALIFLILLTVFNSAPKTGRNGASSRRKQRGSRRRAALVIAVAIALF
ALFANRVAIRMETRLEDDMRFCYMPGIARAITDNWPLGSGLSSFAEIYAPYHAARCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAVVTHAHNVYAEGLLIJGAAPPFYVAFFVLVQLTIFIRGTRRRNYRYASHLGLAAL
LIJCLHSILDESLQIPOCRAMYAVFLAPVITLCLNPPGVERDARKRQRQSSAVVISE
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ETIGLAVVDSLKLTENQEFRATRASLLSSIFGTIRSLVNVSQWFSPTKKEAVIDDGTL
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                                                                                                                                                                                                                                                                                                                                                                                   LVRRLARVIDELQPDVVNTHSLSELTPLIWPMIRKRGIPLVHSLHDFTSMCTNGSLFH
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                                                                                                                                                                              /note-"LPS blosynthesis RfbU related protein --
Methanobacterium thermoautotrophicum (strain Delta H)"
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                                                                                                                             complement 2569. 3645)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3800, .5323)
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complement (3800. 5323)
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ACCESSION

VERSION KEYWORDS

REFERENCE

AUTHORS

JOURNAL

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                    Agrobacterium tumefaciens str. C58 linear chromosome, section 55 of AB009285 AB008689
                                                                                                                                                                                                                                                                                                                                                                    Wood, D. W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G. E., Chen, Y., Wood, D. W., Setubal, J.C., Chapman, P., Okura, V. R., Almeida Jr., N. F., Zhon, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, E., Palmieri, A., Raymond, C., Rouse, G., Saenphimmachak, C., Wu, Z., Gordon, D., Elsen, J. A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon, Ramn, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S. V., Tomb, J., Gordon, M. P., Olson, M. V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-SEP-2001) Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA 98195-7242, USA
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located using Blastx/Glimmer"
                                                                                                                                                                                                                                 Agrobacterium tumefaciens str. C58 (U. Washington).
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Washington)"
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Science 294 (5550), 2317-2323 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative;
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                                                                                                                                                                            AE009285.1 GI:17741958
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RESULT 27
AE009285
LOCUS
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FEATURES

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located using Blastx/Glimmer"
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/note="identified by sequence similarity; putative;
located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"conserved hypothetical protein"
/protein_id-"AAL44366.1"
/db_xref-"GI:17741961"
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/db_xref="GI:17741963"
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/trans1_table=11
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3642. .5918
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10858 CGCCCGCACATCATCGCCTCGACAACCACCGGCCGAAGGGTTCGGCAACGATCGAGGTA 10917
                                                                                                                                                                                               .0918 TGGGCAACCACATCCATCGACGCCATTAGTTCCGGCACATCCGAACGGAAACCAAGGAAG 10977
                                                                                                                                                                                                                                                                                                                                                                                                     SWU52844 20693 bp DNA linear BCT 26-OCT-2001
Serratia marcescens strain N28b waa gene cluster, partial sequence.
U52844
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Submitted (27-MAR-1996) Microbiologia 1 Parasitologia Sanitaries,
Parcultat de Farmacia, Universitat de Barcelona, Av. Joan XXIII s/n,
Barcelona 08028, Spain
4 (bases 1 to 20693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regue, M., Coderch, N., Pique, N., Abitiu, N., Merino, S., Izquierdo, L., Urgell, C., Tomas, J.M. and Regue, M. Characterization of the waa gene cluster involved in core lipopolysaccharide biosynthesis of Serratia marcescens N28b
435 ACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTT----CATTTTCCGAAGGC 491
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Universidad de Barcelona, Av. Joan XXIII s/n, Barcelona 08028,
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Universidad de Barcelona, Av. Joan XXIII s/n, Barcelona 08028,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pique, N., Coderch, N., Abitiu, N., Aguilar, A., Merino, S., Tomas, J.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                     492 ATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGGGCACCTGCCATT
                                                                                                                                                                               552 AACACATCTCCGCTCATTCCCAGGTGTTCTGTCTGCTGACGCGAGACGTGCTTCGTATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guasch, J.F., Pique, N., Climent, N., Ferrer, S., Merino, S., Rubires, X., Tomas, J.M. and Reque, M. cloning and characterization of two Serratia marcescens genes involved in core lipopolysaccharide biosynthesis J. Bacteriol. 178 (19), 5741-5747 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 version replaced gi:4753134.
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/strain="N28b"
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Location/Qualiflers
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/note-"rfaD"
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QPDVVNTHSLSELTPLIWPMIRKRGIPLYHSLHDFTSMCTNGSLFHDGHICDGSSKKC
RAFSYLHRRCCCSVDAVAGYGRDIVERHYRAGFFTHYPESRRYVINNAISPPDAPRPC
TARAPGAPVAPLYFGYLGE TAARGADLLIFALRFLPSGGWRLVMAGRAPDGIEAYOG
KTAGLEYFEPGYVERNRFRGIDCLIYPPLWPEAFGRIYABALLLRGYPPIGBALAGYA
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                                                                                                                                                 DAVVTHAHNYYAEGLITIGAAFPFYVAFFVLVQLTIFITGTRKRRNYRYASHIGIAAL
LLVILHSILDFSLQIPGFAMAYAVFLAPVITLCINPFGVERDARKRORGSSAVVISE
8207. .9421
/gene="atu3558"
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                         GATDIESRIVVTAAIYLLLVPAILMFGPPRÄGAGKVLLAACFLLGALIVQMLLQTSSM
PAMARPNPAWSTAAMFTQIAPAATISLTPADDWLGLWSAALPFGAFWTGLVIFNTDER
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ILLTLATLLHKSLLAPDWAWYRLVPNTLTVPADQKKLITKSVFIGVLAGFSFIALMI
TGSRAGIASSLAALIFILLILTHENSPKTGRNGASSRRKQRGSRRRAALVIAVIANIALF
ALFANRVAIRMETRLEDDWRFCYMPGIARAITDNWPLGSGLSSFAEIYAPYHAARCGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer" /codon_start=1
                                                                                                                                                                                                                                                                    /gene="Atu3558"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
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located using Blastx/Glimmer"
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Pred. No. 9.2e-05;
0; Mismatches 188;
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complement(10623. .11771)
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/protein_id="AAL44372.1"
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/gene="Atu3560"
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COMplement(9476. .10570)
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Best Local Similarity
Matches 178; Conserv
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gene

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AKLFIGVDSVPHHMAAALQTPCVALFCPSKLFFWRPWQATGAVIWAGDFGELDPDDAI
AGTDBRYTALDIPTDAVIAAARSTLA"
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GITRNIKPKDIEDLLFAMEKMLRFVAOHPGDEPLRRLAALMLANCFSEVKSMSKAVYG
YYHYAPATLQILRRAATVCRNSDVPCKKVRQMRYARVDTFLSKLRGRKPR"
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GLAAAIRAVAATDSHLLVVGKDKAEKRYRALAQSIGCGDRIHFMGVQKQTLPFYQAAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mkafllalvrrkyrpdggaerfysralkaleqqddldlnvitrew
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SLKGVWGALLLLALYIGLFFSSFRPQRNALLLSVSASLFYYGLSDVIFFSTEGTVMFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9516. 9598

//gene="waaQ"
8516. 9598
//gene="waaQ"
//gene="waaQ"
//once="complements a non polar Klebsiella pneumoniae waaQ
mutant, similar to WaaQ proteins from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6246. .7340)
/note="Orf7; LPS from a non polar orf7 mutant has reduced
levels of D-D-heptose"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosyltransferase and Waag from Salmonella enterica
serovar typhimurium, and Escherichia coli strains K-12,
R2, R3 and R4; Orf9; LPS from double non-polar orf9-orf10
mutant lacks Gala, has reduced Glc levels and contains
                                                                                                                                                                                               5229 .6209 ./hote-e-orfé, similar to TsrB (WbcK) protein from Yersinia enterocolitica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to Klebsiella pneumoniae C3 putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"putative glycosyltransferase"
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YQAFTQADLTNLRKAGYDKPFRTVAEGVTEYMAWLNNDA"
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KLLSHINCADAVETLVAGGETYQTLSRNAQRYPAEHFNYAQFKAEFDDTLRSFIV*
3991. 5232
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PORTGWRGERKYGLLMDYRYLDKAAPPLAYORYVALAYDKGRVQRADDLPQPLLMPQL
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1834. 2799
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                                                                codon_start=2
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                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="waaf"
785. .1831
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3991. 5232
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                           'gene="gmhD"
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/note-"Best Blastp hit = g1|7433884|pir||E72354 probable hexosyltransferase (EC 2.4.1.-) TM0622 - Thermotoga maritima strain MSB8) g1|4981142|gb|AbD35706.1|AE001736_4 (AE001736) lipopolysaccharide biosynthesis protein, putative [Thermotoga maritima]', score 263, E-value 4.00E-69"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARHDNSKI I IVGDGEERERLEBLITKLHRLERKYYFIGIRTDIPDILNASDVFYLSSD
WEGNPLSVWBAMAAGKPVIATSVGGVPELIQNNITGILVPPKNVNAFSKAMLMLIENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Translation="MFTLIVVLILGLMIVFFEIWRWRKIKFIDFLRGFNIVYFIIFL

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KDINNDFPFLTLSQENTLILGTEKGGIPVDILGAGFFSANIFGVVFIMFCLGMILAL
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SRIKEYVVSEFSFPKEKVDVIFNAVDIDIFKPISELEKKQIREELGWGEEDFVVFIPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKYYRACDVVLIPSITSDGVEEATSLSMLEGMSCGKIVVCTPIGGMKEIIKHGVNGFF
VEOKSEEAIAYIIEKIKEDFYKLDSIRQEARKYIEKNHSYIVHARKFIEVYEKAIK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERIFSNVSNPVLRSLKIAWILYFSTMVVLYADPAILLWDGVYLIFPTIVFLMLYLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forte-refam match to entry Glycos_transf_1, Glycosyl transferases group 1, score 123.5, E-value 3.90E-33" 1350. .2742
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transferases group 1, score 199.9, E-value 4.00E-56"
3886. .4839
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                                                                                                                                                                                                                                                                                          11607 ACAACAGCGATTCTACCAGCACATTGCCAAACCCTTCGCTATCGGAGCTGAGCACCAACA 11548
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Than Y. Xue,Y., Xu,Y., Lai,X., Huang,L., Dong,X., Ma,Y. and Tan,H.
Direct Submission
Submitted (07-0CT-2001) Institute of Microbiology, Chinese Academy
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Boo'O. Than,Y. Tai,W., Xu,Z., Xuan,Z., Hu,S., Dong,W., Yang,J.,
Chen,Y., Xue,Y., Xu,Y., Lai,X., Huang,L., Dong,X., Ma,Y., Ling,L.,
Tan,H., Chen,R., Wang,J., Yu,J. and Yang,H.
A Complete Sequence of the T. tengcongensis Genome
Genome Res. 12 (5), 689-700 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tengcongensis strain MB4T, section 61 of 244 of
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Bao, 0., Xu,Z., Hu,S., Dong,W., Chen,Y., Wang,J., Yu,J. and Yang,H..
Direct Submission
Submitted (07-0CT-2001) Beijing Genomics Institute/Genomics and
Bloinformatics Center, Institute of Genetics and Development,
Chinese Academy of Sciences, Beijing Airport Industrial Zone B6,
Beijing 101300, China
                                                                                                                               382 CATTCTTCTGAATGACATCAGGGATCCCGCCGTCTCACTGGCGATAACGGGCACGCCGG
                                                                                                                                                                                                                                                                                                                                           502 CACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTC
                                                                                                                                                                                                                                                                                                                                                                                             11547 GCGAGGCATGGCGGATAAACGGATTAGGGTTGGCCTGGAAACCGAGGAACAGCACGCGCT
                                                                                                                                                                                                                                     442 AGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCA
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                                                                             Gaps
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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                      Length 20693;
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/organism="Thermoanaerobacter tengcongensis"
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Li,W., Xuan,Z., Yang,J., Ling,L. and Chen,R.
Direct Submission
                      Score 50.6; DB 1;
Pred. No. 0.00034;
0; Mismatches 124;
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/db_xref="taxon:119072"
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/gene="RfaG4"
                      4.3%;
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the complete genome.
AE013034 AE008691
                      Query Match 4.3
Best Local Similarity 50.2
Matches 125; Conservative
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AE013034/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                       3839 TITITACCATTACACTAATATCAAACTCTTTCTCAGCAACTTCCTTAGCCTTTTCTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                 292 TCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAGTGCGGCCGGTCCATGCAGACA
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Stone, N.E., Schnutz, J.J., Cox, D.R. and Myers, R.M.
Direct Submission
Submitted (11-SEP-1998) Department of Genetics, Stanford Human
Genome Center, 85 California Avenue, Palo Alto, CA 94304, USA
Jesses 1 to 199450)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 CATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGC
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                                                                                                                                                                                        gi|3451511|emb|CAA07667.1|
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                                                                                                                                                                                                                                DB 1; Length 8594;
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Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                       Pred. No. 0.0006;
0; Mismatches 139;
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/note="Best Blastp
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                                                                      /note="TTE0662"
7215. .7219
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/gene="RfaG7"
                                                                                                            /gene="RfaG7"
7227. .8462
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       .50E-150"
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SHGC-50921 G33945
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SHGC-51591 G34129
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Best Local Simi
Matches 133;
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LKNLLIIPKGLVVSEILKKRKINHIHAHMASTPETIKHPLRVVEIRKILKHSGSLGKI
LKNLLIIPKGLVVSEILKKRKINHIHAHMASTPETLAYIASELFGIPWSFTARRWDIA
RRALLIAVPROFYKRGYINTINHIHAHMASTPETLAYIASELFGIPWSFTARRWDIA
LEDRIFFKGQLPHDELIELSTVKKVIETQNCNYTCXFFGKGLLEDELKTJYTQLN
STNTGGIPELLEGGAGIIVEGKNSDELAKAIMKINDEKLREELGEKGFEKIEFUT
SKIVEELLXLMGNN*
                                                                                                                                                                                                      /transl_table=11
/product="conserved hypothetical protein"
/product="conserved hypothetical protein"
/protein_id="aaM23925.1"
/db xref="GI:30515647"
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/translation="MRYVRILSKYLRILLGKSALHVNQGIGKIYSKEGIKGYYNDLTL
/translation="MRYVRILSKYLRILLGKSALHVNQGIGKIYSKEGIKGYYNDLTL
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TIFNALCKIGKDITIVMPLHPRTKAALLREGLYEKVSEKLKIIEPVGYLDMVKLEKNA
KLIITDSGGVQKEAFFYKVLCVTLREETEWVELVDLGWNYLVPPDCEKFIEESIRKVL
                                                                                                                                           score
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DLMLLPVEKGGTARYVNDKLFLEEVVESKPVLILNGWIFAVFGLYDIFKATSDGRYKE
ALQRTLDTLKDELYKYDTGYWSYYDQCGNLASPFYHKLHIALLEVLYELFNTIEFKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Best Blastp hit = gi|7470136|pir||577339
pypthetical protein s111723 - Synechocystis sp. (strain
PCC 6803) gi|1655251|dbj|BAA17442.1| (D90906) hypothetical
protein [Synechocystis sp.], score 117, E-value 3.00E-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"predicted glycosyltransferases"
protein_id-"AAM23926.1"
/db_xref-"GI:2051548#
/translation-"MKGMKIAYITSQTPYGKGEQFILPEILEVIKKGHDVVVIPVRPE
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'AJ007747) putative UDP-N-acetylglucosamine 2-epimerase
'Bordetella bronchiseptica], score 381, E-value 1.00E-105"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKIVTIIGTRPQFIKAATVSRKIKDFNDMKEIIVHTGQHYDDNM
SDIFFKELEIPQPDYYLGIGSGSHGVQTAHMLEKIEDVLIKEKPDVVLIYGDTNSTLA
GTLAASKLQIPVAHVEAGLRSFNRKMPEEINRIVADHVSDLLFAPTRVAVNNLINEGI
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/gene="WecB2"
/note="Pfam match to entry Epimerase_2,
UDP-N-acetylglucosamine 2-epimerase, score 512.8, E-value
                                                                                                                                 (AF330049) D-glucuronyl C5-epimerase [Mus musculus], 96.3, E-value 5.00E-19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rfag6"
/note="Pfam match to entry Glycos_transf_1, Glycosyl
transferases group 1, score 154.5, E-value 1.80E-42"
                                                                                                                 gi|13442978|gb|AAK26246.1|
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/protein_id="AAM23927.1"
/db_xref="G1:20515649"
                                                                                                                                                                                                                                                                                                                                                                                                            KEKWESYLSNKFKRTRAFIVKAYOKIKEPGEVVLIK"
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                                                                                                              /note="Best Blastp hit =
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/gene="WecB2"
/note="Best Blastp hit
       /gene="TTE0659"
/gene="TTE0659"
3901. APP
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/gene="RfaG6"
/note="TTE0660"
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/transl_table=11
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                                                                  3901. .4839
/gene="TTE0659"
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/4852. 607
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(6099. 7111
gene="TTE0659"
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/gene="RfaG6"
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AP000007 253505 bp DNA linear BCT 06-APR-2000 Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position
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Kawarabayasi,Y., Sawada,M., Horikawa,H., Haikawa,Y., Hino,Y.,
Yamamoto,S., Sekine,M., Baba,S., Kosugi,H., Hosoyama,A., Nagai,Y.,
Sakai,M., Ogura,K., Otuka,R., Nakazawa,H., Takamiya,M., Ohfuku,Y.,
Funahashi,T., Tanaka,T., Kudoh,Y., Yamazaki,J., Kushida,N.,
Oguchi,A., Aokl,K., Nakamura,Y., Robb,T.F., Horikoshi,R.,
Masuchi,Y., Shizuya,H. and Kikuchi,H.
Complete sequence and gene organization of the genome of a
hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3
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AP000007 AB009464 AB009465 AB009521 AB009522 AB009523 AB009524
AB009525 AB009526 AB009527 AB009528 AB009529 AB009530 AB009531
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                                                                                                                                                                                 Bacillus clausii
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                  others
                                                                                linear
                                                                                                                                                                                                                             Berka, R. and Clausen, I.G.
Methods for monitoring multiple gene expression
Patent: WO 0229113-A 6118 11-APR-2002;
Novozymes Biotech, Inc. (US); Novozymes A/S (DK)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.6; DB 6;
Pred. No. 0.00075;
0; Mismatches 124;
                                                                                DNA
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Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                            /organism="Bacillus clausil"
/db_xref="taxon:79880"
149 c 199 g 208 t
                                                                           783 bp Dr
Sequence 6118 from Patent W00229113.
AX437703
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Best Local Similarity 49.8%;
Matches 123; Conservative
                                                                                                                                                               Bacillus clausii.
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                                                                                                                                                                                                74 TCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAATGTGATAAATTACTC
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Methods for monitoring multiple gene expressi.
Patent: WO 0229113-A 1695 11-APR-2002;
NOVOZYMES Biotech, Inc. (US); NOVOZYMES A/S
Location/Qualifiers

    .1135
    /organism="Bacillus licheniformis"
/db_xref="taxon:1402"
    251 c 278 g 279 t

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                                                                                                                               Score 49.6; DB 9;
Pred. No. 0.0012;
0; Mismatches 99;
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AX433280
AX433280.1 GI:21658084
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                                                             /clone="RP11-448G15"
a 46671 c 45223 g 52721
                                                                                                                                                                                                                                                                                                                                                                                                 AAACCGGTACTCAATATCTTCTCTGGCG 281
                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
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Bacillus licheniformis
                                                                                                                                Match 4.2%;
Local Similarity 52.4%;
les 109; Conservative
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                                                                                                                     Submitted (11-70N-1998) Yutaka Kawarabayasi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya ku, Tokyo 151-0066, Japan (E-mail:genomeO73@iite.go.jp, Tel:+81-3-3481-8951, Fax:+81-3-3481-8424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robb, T. F. is at the Center of Marine Biotechnology, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maryland, Baltimore, MD, USA.

Horikoshi, K. is at the Japan Marine Science and Technology Center, Yokosuka, Kanagawa 237-0061, Japan.

Masuchi, Y. is at the University of Tokyo, Meguro, Tokyo 153-0041,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Japan.
Shizuya, H. is at the California Institute of Technology, Pasadena,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The other authors are at the National Institute of Technology and Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan. All the sequence with length 100 codons or more between ATG or GTG and stop codon are defined as CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homology analysis is performed by Smith-Waterman algorithm against GenBank and GenPept release 103; EMBL release 52.0; Swissprot release 34.0; PIR-Protein release 54.0; and OML release 29.5. E-mail address for comments and questions: genomeOrl@alte.go.jp Restriction map, ORP organization, sequence alignment and more information are available at W.W.W. site of Biotechnology Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 CCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAA 471
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                                                                                                                                                                                                                                                                                                                                                   AB009464-AB009465, AB009521-AB009531: submitted (10-DEC-1997)
Rawarabayasi, Y. is officially affiliated with the National
Institute abloscience and Human-Technology, Tsukuba, Ibaraki
305-0046, Japan.
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                                                     2 (bases 1 to 253505)
Tanaka,T., Kawarabayasi,Y. and Kikuchi,H.
Direct Submission
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AL391406 AL645882
AL391406.1 GI:9857143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="1485001-1738505 nt. 56827 c 47619 g 74625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:53953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ://www.bio.nite.go.jp/
DNA Res. 5 (2), 55-76 (1998) 98344137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Matches 10
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DEFINITION
ACCESSION
VERSION
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                              MEDLINE
REFERENCE
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       JOURNAL
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-478(1994) and the Frameelot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                correct initiation codon. Where possible we choose an initiation codon (atq, atg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 2046 lies restriction fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                  Actinomycetales; Streptomycineae; Streptomycescaeceae; Streptomyces 1 (bases 1 to 35576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
                                                                                                                                                                                       Redenbach, M., Kieser, H. M., Denapaite, D., Eichner, A., Cullum, J., Kinsshi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome

Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-AUG-2000) Streptomyces coelicolor sequencing proje
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the BBSRC and Beowulf Genomics Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
3 (bases 1 to 35576)
Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission ctrantomyces coelicolor sequencing
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptomyces coelicolor A3(2)"
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/clone="cosmid 2D46"
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complement(142. .147)
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Brown, S.P. and Harris, D.
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CDS

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17425 GGCGGCGTCGCCCATGCGGGCGTCAGATCGGGGTTGTCGGCGAAATCGCGCAGCACGCG 17366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative hydrolase"
/protein_id="CAC04027.1"
/db_xref="Eq1:985718"
/db_xref="SPTRRBL:08FCH8"
/translation="MVRRPLGNHHHGHDTLLVTSDTDQTEPVSERTGRDEQSEALRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVGARVVLMDFDGPICRLFAGYSADRVAGELVDWLERIGLKELLTGEEGVÄPDPHVLL
PAVDRHRRSDLVABFEERIYEBELRAVPTAMPTAÄDALIRWASALGYGLAVTINNS
PRVVSEYLETREDLLGCEAPHTYGRTGDPHLIRPDHGLIRRALSARAGARPARALMYGDS
ASDVTAARRAGVPFLGYGHNERKTKLLKQAGADTVVDSLEPVLRLLWENGTPAPA"
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                                                                                                                                                                                                                                   ELAEEFGVERGTVRQALRALQEDGLLTNVSKGSPPRIAEPATPRAEPQPTMVALGPRL
AEAFAAPHVRVDVVCHTSETLMLALSEPLRLIHEGRIHPESIDFRVLMPSRDIALAFP
                                                                                                                                                                                                                                                                                                            VLVEDEEDDPVHQRWLQMRNAQARVLQHNLHAVRSTHRVDVRIAFRALPFTPPMKLYL
LNGEEALLGYYMLTRREEFESTESRTLQMYDALGSOSLLFSFLNRTGHRDAVFVEESQKW
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Agene="25CD46.05"
/note="Pfam match to entry PF00702 Hydrolase, haloacid
dehalogenase-like hydrolase, score 37.40, E-value 3.2e-07"
                                                                                                                                                  /db_xref="SPTREMBL:Q9FCH9"
/translation="MVVTQENVSVNGSRRLSSQEIADVLRERIRGGDLRAGDRLPTQA
                            /product="putative GntR-family transcriptional regulator"
/protein_id="CAC04026.1"
/db_xref="GI:9857147"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-#25CD46.05, possible hydrolase, len: 273aa; weakly similar to many proposed phosphataes eq. TR:CAB84916 (EMBL:AL162756) putative phosphatase from Neisseria meniagitidis (235 aa) fasta scores; opt: 195, z-score: 238.2, E(): 8.8e-06, 29.5% identity in 237 aa overlap. Contains Fram match to entry pr00702 Hydrolase, haloacid dehalogenase-like hydrolase. Note possible alternative downstream translational start codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry PF00392 gntR, Bacterial regulatory proteins, gntR family, score 69.30, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 GGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="2SCD46.05"
/note="SCO4191"
/1016="SCO4191"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2363. .3184
/gene="2SCD46.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="2SCD46.04"
                                                                                                                                                                                                                                                                                                                                                                                             FDALWETITTDMTLS"
1599. .1751
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Best Local S:
Matches 120
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AC092541
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/gene="2SCD46.04"
/gene="2SCD46.04"
/note="2SCD46.04"
/
                                                                                                                                              /Jote="25CD46.02, possible GntR-family transcriptional regulator, len: 303aa; similar to many eq. TR:Q9R102 (EMBL:AJ243257) RorA protein from plasmid psNal of Streptomyces natalensis (245 aa) fasta socres; opt: 175, z-score: 204.2, E(): 0.00069, 28.2% identity in 238 aa overlap. Also strongly similar to nedghbouring CDS 25CD46.04 fasta socres; opt: 1074, z-score: 984.2, E(): 0.57.6% identity in 302 aa overlap. Contains Pfam match to entry PF00392 gntR, Bacterial regulatory proteins, gntR family and helix-turn-helix motif (Score 1967 (+5.89 SD)) at residue 46-67. Note possible alternative downstream translational start codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="2SCD46.03c, unknown, len: 62aa; strongly similar to endighbouring CDS 2SCD46.03c faata scores; opt: 169, z-score: 236.7, E(): 1.4e-07, 51.1% identity in 45 aa overlap. Hydrophoblc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref-"SPTREMBL:Q9FCIO"
/translation="MVVEPBHAPVNRERPORPQATHREVADELRARIRSGRLRPGQR
/translation="MVVEPBHAPVNRERPORPQATHYBOPYGPQSGPBARPM
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PTTVALASRIAAARAABEHVBIDALCLLSVSLTLALGEPLSQIHAGRLKPAKVUNVULL
PSGDIDLARPVAVSGGAAGGPVHERWIAARRAAGQVLRHNLLSLRATHGIDVRVSFRA
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DGVFVKQSRLWFDALWGTISSELVLAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative GntR-family transcriptional regulator"
/protein_id="CAC04024.1"
/db_xref="GI:9857145"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Repeated degenerately at 1210. .2414. This DNA repeat manifests as a duplication of a pairs of CDSs su that 2SCD46.01c is similar to 2SCD46.03c and 2SCD46.02 similar to 2SCD46.04."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF00392 gntR, Bacterial regulatory proteins, gntR family, score 64.70, E-value
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/protein_id="CAC04025.1"
/db_xref="G1:9857146"
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/gene="2SCD46.03c"
/note="SCO4189"
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/gene="2SCD46.03c"
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/gene="2SCD46.02"
                                                                                                                 /gene="2SCD46.02"
/gene="2SCD46.02"
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                            /note="SC04188"
289. .1200
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Submitted (16-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9297)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 0% Sequencing vector: M13; 0% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 638 bases at least Q40 Consensus quality: 7446 bases at least Q30 Consensus quality: 7999 bases at least Q30 Insert size: 173000; agarose-fp Insert size: 8797; sum-of-contigs Quality coverage: 0.06 in Q20 bases; sum-of-contigs Quality coverage: 1.23 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 1143 bp in length
gap of unknown length
contig of 1588 bp in length
gap of unknown length
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4824: gap of unknown length
6374: contig of 1550 bp in length
6474: gap of unknown length
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8230: gap of unknown length
9297: contig of 1067 bp in length
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1244. .2831
/note="assembly_name:Contig20"
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/note="assembly_name:Contig22"
4825. .6374
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/note="assembly_name:Contig23"
6475. .8130
                                                                                                                                                                                   The sequence of Homo sapiens clone Unpublished
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Corganism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="RPCI-11"
/clone="RPI1-203G11"
                     AC092541.1 GI:14719349
HTG; HTGS_PHASE1; HTGS_DRAFT
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4824:
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Waterston, R.H.
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Pyrococcus furiosus DSM 3638.

Pyrococcus furiosus DSM 3638

Archaea; Euryarchaeota; Thermococci; Thermococcales;
Thermococcaceae; Pyrococcus.

(bases 1 to 10991)

Madder, D.L., Weiss, R.B., Dunn, D.M., Cherry, J.L., Gonzalez, J.M.,

DiRuggiero, J. and Robb, F.T.

Divergence of the hyperthermophilic archaea Pyrococcus furiosus and
P. horikoshii inferred from complete genomic sequences
Genetics 152 (4), 1299-1305 (1999)
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Robb, T., Maeder, D.L., Brown, J.R., DiRuggiero, J., Stump, M.D.,

Yeh, R.K., Waiss, R.B. and Dunn, D.M.

Genomic sequence of hyperthermophile, Pyrococcus furiosus:

implications for physiology and enzymology

Meth. Enzymol. 330, 134-157 (2001)

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Submitted (12-FEB-2002) Human Genetics, University of Utah, 20
South 2030 Bast, Salt Lake City, UT 84112, USA
Location/Qualifiers
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the Pyrococcus furiosus genome
                                                                                                                Length 9297
                                                          508 others
                                                                                                            Score 47.4; DB 2;
Pred. No. 0.0032;
0; Mismatches 207;
/note="assembly_name:Contig24"
8231. 9297
//note="assembly_name:Contig6"
//1835 c 1804 g 2548 t
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AE010283.1 GI:18894070
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The complete sequence of
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Weiss, R.B.
                                                                                                        Query Match
Best Local Similarity 34.9 Matches 111; Conservative
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DKRIVKYPGANRFKEVKENYLKLARHHHLSSNPLPIVJEKAVNIAKNIGLITVSPDPGEM
EVENHIEERTDLILMMNEDEFKRYGSLEKITELKSRIAIATINGGGALVRDENGNYE
IRGLSAKAIDTJGGGDSFDAGFIYGYLNGWDVKDSAKLGMLAYLTVQKVGARSAVIP
LDEVKKIAKELGLDLPPQ"
COMPLEMEN (7471. . 8292)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mgvTeelealkgvarknwkiflsykawfvsdilmgfffagnall
iglgltgkrtsealaelfgysdylffailgfwvlafgmtfwsgfvwsivdelyagtle
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AFGMIGLGLMAAGIVIYLKDPGPFVNILEMLVFALSGAMYPVKILPKPLQIMAKLLPY
APTTEAVRKVALVGLSKSAGEIMYLSLISIIYTLLGVLTYRWABRRAREIGLKSY"
                                                                                                                                                                                                                                                                                                               /translation="MKKRREFSLIAFLISLAYLYRSIDLKELPSAISEANYFYLTVAF
LLSILTVLLGALRWYLVMRWYONTSFRRTLQAFISGYTLAAVLDFTLGHITKWKLVGG
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FYRLAENSLAFGIAIEIITVLSFALTHEGFTKLGFFGLGIILLAFVYDKIFHRAALIV
FKLWENKLGIKKVPNILKNWYQRLTGKKKBKLTFYSTFLISFAVIILQYFGLVFY
GKAFLLDIPIKKAFYAFIMSVVFASLSGIPSGVANEFGILVGIGSSTRAALTAFIYK
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/translation="MKLDVICMGNLNYDITFMLERFPEFHEKVNAKKVYTGLGGSAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Function Code: 14.1 Transport and Binding Proteins:
                                 'note="Function Code: 14.1 Transport and Binding Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mhnlatklrerghevgivtnnrvtgkerelekygidlikipgvv
SPLLevnitygikSSElneplnnfDvihSHHAFMPLalkavkagrtmekatlltyhSi
                                                                                                                                                                                              (ATP-binding protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /going Function Code: 3.2 Cell Envelope: Surface polysaccharides, lipopolysaccharides and antigens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="PF1887"
/note="Function Code: 16.1 Conserved Hypothetical"
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/transl_table=11
/product="conserved membrane protein"
                                                                                                                                                                                                   transporter
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/protein_id="AAL82009.1"
/db_xref="GI:18894076"
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/protein_id="AAL82011.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIFQYQYSIIGAFVFYKLLSGGNESSSS"
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complement(8279. .9046)
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                                                                                                                                                                                          /product="putative ABC
/protein_id="AAL82008.1
/db_xref="GI:18894075"
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/transl_table=11
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/gene="PF1886"
6593. .7477
/gene="PF1886"
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/gene="PF1885"
5490. .6566
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/gene="PF1885"
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                                                                          General"
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VDVAEIVRNRFLKDIVDIKEIKIGTEELPTADGRTINTSTIEIVLERKV"
complement(1161..3551)
/gene="PF1882"
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epamyeervgevwrepfydifdngdefyltaelpgyrkedikvrytedtyyieatykr
ekeleregavrieryffgyrrairlpeeyiperakakynngyleirypkkhytkkese
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VAEKAVRESVIDTNNVDKIIQKLRRNYRKALREGIVDSTEDFELILLAKEIDGIIVSA
DVGILTWAEKMGIKWVDAFKFKELLDELVEKVESEKERK"
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PAIIFIDEIDAIAPKREEVTGEVEKRVVAQLLTLMDGLKSRGKVIVIGATNRPDAIDP
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DVIDRAIDQVSKAKEEEIQQVLKRISQDLYEEVKARLIDKLLEELAEVTYGFVGADLA
ALAREAAMAALRRLIREGKIDFEAETIPREVLEELKVTRRDFYEALKMVEPSALREVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MIRFILDTSIFVNPDVRKKFGNTPTEAMKTFLKYAEKLFGKVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSEKKKEVKLKVASAYQRDVGRGIVRIDRETMRELGISPGDVVE
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TRGTDVNRVTDRIINQLLTEMDGIVENSGVVVIGATNRPDIIDPALLRPGRFDRLILV
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                                                                                                                                                                                                                                                                                                                   /note="Function Code: 12.3 Transcription: RNA processing" 
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEIPNVHWDDIGGLEEVKQQLREAVEWPLKYPEAFRAFGITPPKGILLYGPPGTGKŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaa family"
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/gene="PP1882"
/note="Function Code: 4.2 Cellular Processes: Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Function Code: 16.1 Conserved Hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                               Product="mRNA 3'-end processing factor homolog'
Protein_id="AAL82004.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="cell division control protein 48, /protein_id="AaL82006.1" /db_xref="GI:18894073"
1. .10991
/organism="Pyrococcus furiosus DSM 3638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
Product="small heat shock protein"
/protein_id="AAL82007_1"
/db_xref="GI:18894074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAL82005.1"
/db_xref="GI:18894072"
                                                                                                                'db_xref="taxon:186497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3723. .4226)
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/gene="PF1881"
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/gene="PF1881"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:18894071
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                                                                      /strain="DSM 3638"
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/transl_table=11
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/gene="PF1884"
4535. .5449
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                                                                                                                                                                                              /gene="PF1880"
                                                                                                                                                                                                                                    l75. .774
/gene="PF1880"
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I (bases 1 to 10148)

Elsen, J.A., Malson, R.E., Paulsen, I.T., Heidelberg, J.F., Wu, M.,

Elsen, J.A., Deboy, R., Gwinn, M.L., Nelson, W.C., Haft, D.H.,

Holt, I., Umayam, L.A., Mason, T., Brenner, M., Shea, T.P., Parksey, D.,

Nierman, W.C., Feldblyum, T.V., Hansen, C.L., Craven, M.B., Radune, D.,

Vamathevan, J., Khouri, H., White, O., Gruber, T. M., Ketchum, K.A.,

Venter, J.C., Tettelin, H., Bryant, D.A. and Fraser, C.M.

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium

L. Proc. Natl. Acad. Sci. U.S.A. 99 (14), 9509-9514 (2002)
                                                             /translation-*MEPRYPLRVISSILVGLVFLLQFVYFGQAILGGRFSRLLEBATG
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complement(9079. .10035)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"daunorubicin resistance ATP-binding protein drrA"
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/note="Function Code: 15.2 Other Categories: Drug
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Chlorobium tepidum TLS
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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llarity 60.5%; Pred. No. 0.0033;
Conservative 0; Mismatches 51; Indels 0;
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AE012967.1 GI:21648252
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                                                                                                                                                                                                /translation="MQGHAISIQPRCVITPMLYAFEKLATGQCPAYSAFDSIYDTYFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1183 GATGCCCTCCTCCAGCGCAGGCGCTCTCTCTCGCGGAAAAGTCGAGAATCCCGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 CCATGCAGACACCATCCCCCACGGGTAACAGCGTCCCTGTCACATCTTCTTGAATGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAAATCGCGCAGTGCGCCGGT
                                                                                                                                                                                                                                                                                                      /note="identified by match to PFAM protein family HAM PF01661"
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Bacillus clausii
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Pred. No. 0.0046;
0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.0%; Score 47.2; DB 1; Length 1
Best Local Similarity 50.4%; Pred. No. 0.0038;
Matches 115; Conservative 0; Mismatches 113; Indels
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a 150 c 204 g 203 t
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Sequence 6111 from Patent W00229113.
AX437696 1GI:21662504
                                                                                                                                                                                                                                           complement(6837. .7355)
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                        6681. .6824
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Best Local Similarity 59.5%;
Matches 78; Conservative (
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COMPLEMENT(5910. .6491)
                                                                                                                                                     EVICDNVEDGQEIMIAKGGRGGWGNQHFATATRQAPRFAQPGEPGEEYELEMELKLMA
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VVITKMDIAPEDFTWPELEKGVKVLAISSVAGGELKALKDELWRQVSLQNQSPSEHAG
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6475. .6603
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                                                                                                                                                                                                                                                                                                                                                                         /note="identified
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2569. ;3042
4569-**RA318**
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complement (3069. .3881)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="PA3219"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4857. .5192
/gene="csaA"
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/gene="csaA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalkk, D.J., Lagrou, M., Garber, R.L., Gollter, S.L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.M., Folger, K.R., Kas, A., Larbig, K., Lim, R., Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
Nature, 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein"
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                                                                                                                                                                                                                                                       AE004745 11884 bp DNA linear BCT 30-AUG-2000
Pseudomonas aeruginosa PA01, section 306 of 529 of the complete
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SMPELLVLSFTALVTGGLRLLGMALLYSASSALLVAVLVAPPELLGWPFVAAVSILF
SGLYICITARFGHQGRLRAVOVROETARGDERARLARNLAKYLSPOWEMIFSGKKS
VRLETQRKKLTVFFSDIRGFTELSEELBARALTDLLNWYLNEWSKIALKYGGTIDKFV
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573 ATTITIGICGCGATCACAGGIACCCCGCAIGCCATCGCTICAAGCGCCCACTAAACCAAAG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .11884
/organism="Pseudomonas aeruginosa"
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/transl_table=11
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/gene="PA3216"
102. .419
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636. .2027
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/gene="PA3216"
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/gene="PA3217"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
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AE004745.1 GI:9949336
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                                                        474 GCTTCATTTTC 484
                                                                                        513 CTTTCTTTTC 503
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Methanothermobacter thermautotrophicus str. Deita H.

Methanothermobacter thermautotrophicus str. Delta H.

Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;

Methanobacteriaceae; Methanothermobacter.

E 1 (bases 1 to 11142)

Smith, D.R., Doucette-Stamm, L.A., Deloughery, C., Lee, H., Dubols, J.,

Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R., Gilbert, K.,

Harrison, D., Hoang, L., Kaagle, P., Lumm, W., Pothier, B., Qui, D.,

Spadafora, R., Vicaire, R., Wang, Y., Wierzbowski, J., Gibson, R.,

Jiwani, N., Caruso, A., Bush, D. and Reeve, J. N.

Complete genome sequence of Methanobacterium thermoautotrophicum
delta: functional analysis and comparative genomics

L J. Bacteriol. 179 (22), 7135-7155 (1997)
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KTYVSOLTVIYMLVAAMGAPELMDRLERVPEFMERALEDEDGIKELAATGSDVSDFFF
IGRGFAYPTALEGALKLKEITYIHGEGYAAGELKHGPLALIDNGVPVVAISPFGPCHD
                                                                                                                                                                                                                                Methanobacterium thermoautotrophicum from bases 114371 to 125512 (section 11 of 148) of the complete genome. AE000805 AE000666 AE000805.1 GI:2621213
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Submitted (10-AUG-1997) Genomics and Technology Development, Genome
Therapuetics Corporation, 100 Beaver Street, Waltham, MA
02154-8448, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="glittamine-fructose-6-phosphate transaminase"
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DLRVTDMEGNTVEKEVHSIDWSADMAEKGGYDHFMLKEIHEEPSAVRDTLFEWDEVLG
VVEEIGEVERICFVACGTSYHASLVGKYLFESLLGIPTDVILASEFRYSAGALNDRTL
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101. 1873
//gene="MTH171"
//gene="MTH171"
//note="Function Code:5.01 - L-Amino Acid Metabolism,
Alanine--aspartate and glutamate metabolism; similar to,
gp_new:GI:e315045:g2104357, p()=1.7E-126, pid=45%"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Methanothermobacter thermautotrophicus
Delta H"
                                                                                                        2332 CACCAGCACCGAGGCCGCCGGTAGGC 2358
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/db_xref="taxon:187420"
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                                                                             494 GACCACCACACTGGCAATCCGGTAGAC
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/gene="MTH171"
101. 107.
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                                                                                                                                                     /product-"acyl carrier protein phosphodiesterase"
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IGFVGIHDVTFIHAEGMNMGPEFREKGLARARERMRQALETDTSLCVPLPTLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEQLGVPLLRIDGRKAVLTEAGEVILRRSRQLVKQAGQLEELAHHMEĞGWEPFEVRLVV
DAAVPTARTVRSLSARMPGRGCRVLIRBEVLSGVEEALIQGAADLALSGLIPGHLG
ADLSVVEFVAVAHPDHPLHRCLRELTHQDLFTQMQVVIRDSGRLQPRDHGWLGABÇRW
TVGSLATTAATPVGULGFAKLPRHITERELOSGQLKPLPLSGGGGVRQSRFYLTRKEK
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AILLTNLGGQAAECTAVFRNGPETPKVRRGVIQPGQNSNFTAQFGRDIIKLRIKLICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation-"MPDFQHRDCTLVYDDHPGPTERAPVLLLHGLGSSARDWEYQLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQLACDRPDLLRSLTIVNSTPEVIPRKPREHLEVAKRKLLSRLLSLRTIGRALGRLLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"probable transcriptional regulator"
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Best Local Similarity 57.1%; Pred. No. 0.0083;
Matches 84; Conservative 0; Mismatches 6
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                                             complement(6206. .6847)
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                                                                                                                                                                                                                                                                                                                                                                                complement(6994. .7311)
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                                                                                                                                                                                                                                                                                                                                        complement(6994. .7311)
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7511. .8440
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/gene="PA3226"
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256. .9819
                                /note="PA3223"
                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                /gene-"PA3224"
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/gene="ppiA"
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complement(1927. .2925) /gene="MTH172" complement(1927. .2925) /gene="MTH172"

gene

CDS

CCCGGTCACGCCCTGCTGCAATACATCCAGCGCCCCGGCACGCCGAAGGCCGCCACCGG 2271

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434 CACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCAT 493

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                                                                                                                                                                                                                                                                                     SVDFIKSNFSEYLGDRIILIENHENLGFAASNNQGIRIALDDPQCRYVYCLNNDTEYL
PDFIENLILAAGDDERVGSYQARMIWGQNRKLIDSAGLEYSLNGLGFNRGAYEPVENF
PRARAILGCCAGACLYRREALBDVEYNDAEYFDEDFRAYFYBDFDLALRIRSAGWDSLYA
PDATYYTYRGGTNPFISDFYYHWRNYTWFFIKNNPADLLLAACLPLEYLTIGYLL
NIKRGKLIILRAKYDAYRGIGRYIRKRRALKRYPESEIKEYLTWRWSVKVPSPQED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGPMRILIVSDFFVPHYNGGGERRYFEIARRLVERGHVVDVISM
GIHGVGEYEEVSGVRVHHLGPRIRKPPLRGPLDFIRFWAAAFRWVMTHDYDIIDAQTY
APLLPAFLASRIHGTPMVATIHDVSSAHGDQWLQSSKTATILERVLMRLPYDGVITVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSTASALTELHGRNPDGIHIIPNGVDPELIDSVTPATGNYIIFVGRLAPHKHVDHLIE
VFSKLVIDFPDLRLEIIGDGVERARLKAMVDECGIRDSVTFHHNLSYPEVISRIRGAR
VLVLPSTREGFGMVLAEAGACGVPAVAYRSGGVVEVIDDGENGFLVFPCDKEALHDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSRGSDRTQAHYLLTGLTLPVIAGVLTDLVLPAAGMAVPSLTDPSAALGVSIIAYGVM
RFRLPILSPLNAAMDIVRNMNTFLIITDLGLNIHYVNPATERLTGRRAAEFSGRKVTE
VLKFDELSTGSIMESRLRGKDEWIPVIVSAGHVHGSGGEHLGLLFTGSDMRPILEMEE
KLRRREDRLVLLTEHWADGLGEFDRDFNFRYLSPSVKKITGYDHEMLTGMSALDFMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHPDDTEEVKKLILTRGEGHRATFRIRRPDGNYRWVEYYDRPIRTDGDIEGYYFGLRD
IHEHKLAEEALIVSKEKFRELFRNMRSGIIAVESDGKGFRVKSMNPAAERMEGYSCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQGMDLQEALPEIWNSPIRRALQEIRETGEAIHCPEVECGEGWFDVHLHQLSTGEVVI
TCDITLRKOYSDELAASLERERALLESHYHHWYNRPVISSIINLQLDDAEDPAPLR
DLOSRIQSMALVHELLTSERDLTSIDMGRYTERLTSSIVNSHHNGEIEVEVAVGDITL
PLETAIPLGIIINELVTNSFKHAFTSGGMISVELEEHGGEFTLTITDNVVGLPPDFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MNPMAIISITAFVVALVSGVYIFVKNPESRFNRALLLFSALIAY
LSLTDFGLYISESYMMADFWVRMGFLWPIVVPVILHMVLLFTGRRPTMPLLAVIYAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVIAALELTTDLITAGPIMTSWGWTFSAAENSLPYQISNIWGFIIASVAIILVALHWR
                                                                                                                                                                                                                                                       /translation="MPETYIITPNLNGVSFLEVYFRSLLRQTYEDFRVVFIDNGSSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Function Code:8.02 - Metabolism of Complex Lipids,
Inositol phosphate metabolism ; similar to, pir:LN:F64500
AC:F64500, p()=9.6E-29, pid=27%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="72 bp direct repeat includes part of MTH174 (sensory transduction histidine kinase - paralog fam. 1); 83% ID to interval 400218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="85 bp direct repeat includes part of MTH174 (sensory transduction histidine kinase - paralog.fam. 1); 81% ID to interval 228380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
/note="Function Code:14.01 - Unknown, Conserved protein; similar to, gp:GI:g1666509 LN:LIUG1226, p()=8.6E-16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paralog.fam.
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/note="79 bp inverted repeat includes part of MTH174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of MTH174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Function Code:12.12 - Cell Processes, Broad regulatory functions; similar to, gp:GI:g1652472 LN:D90905, p()-1.1E-36, pid-17%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LLISDDELRDRMGSQGRKKVEEEFIWDRVVDEVERTYSFIIARKNTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="LPS biosynthesis RfbU related protein"
/protein_id="AaB84679.1"
/db_xref="GI:2621216"
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complement(6003. .6074)
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/note="79 bp inverted repeat includes part
(emsory transduction histidine kinase - pa
86% ID to interval 4087"
                                                                                                                                                           /product="conserved protein"
/protein_id="AAB84678.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="sensory transdu
/protein_id="AABB4680.1"
/db_xref="G1:2621217"
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2945. .4093)
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/gene="MTH173"
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/transl_table=11
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/transl_table=11
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/gene="MTH174"
4263. .6620
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/gene="MTH174"
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TDASSVTVDMVEISAGTMATALIVPSPNPAHKIVKGAYEDFILLSEGILSIKTSPPAPS
GIELRVHCGDARAVVPLLERRYYDAIFLDAFSPRVAPELTYTVEFISILAGYLKKRGVL
ATTSAAPRRAALIEAGFHYGGPPYGKSGGTLASMDPRWYKPLDMRDERMIALSD
AGIPYRDPELSADAILEIMGRRYPERMSARGYTRISSARVTPLILGSEQVEGRTGRRYR
RNLSRIGIDDPSGPEALYIICPQMDECICGCGEDRPASSRDKVISMRRRAMDLVNLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Function Code:10.07 - Metabolism of Macromolecules, Aminoacyl LRNA synthetases and tRNA modification; similar to, pir:LN:D64354 AC:D64354, p()=1.4E-121, pid=37%" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Function Code:14.01 - Unknown, Conserved protein; similar to, pir:LN:F64383 AC:F64383, p()=1.4E-41, pid=278" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MALTPRGDVLRTVMDYLEIESRDSVDRRRDLWRSISDKFIRTAD
GSYTLKSEAGEAMHTRVGALTEAIEKFVKPTVSGIKDDLRVLDLCSGLGYNTAALLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLKRVKEHLGERLALVAPSRRPYSSSLPARIGGFSSLRPQSGGPWRVVVDLPPGIIP
ELEDOYYPHAGSDAPGIMDLOGEEFIRGINRDLMOGDAIVDDALCSELGIELPYKYMG
EVETTVDDLDKVRWYADYQFGGAGELLFTDDVRI BESRNTGKIRHIYAGDELCTMR
ASDCLLVLGABGAVRLHKGTDYPAMRVAVNEBSEPFARKGKSVFAKFIIDCDNNIRAN
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DSGSFQLSEYGDIEVENPEIIRFQDEIGTDIGTSLDIPTPPGVSHRRAIEEVEVTLER
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VDAVLSSVSELPPSRPRHLMGAGHPMLFALAVSMGCDLFDSAAYILYAEDDRLLSTEG
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                                                                                                                                                                                                                    /note="68 bp direct repeat includes part of MTH174 (sensory transduction histidine kinase - paralog.fam. 1); 87% ID to interval 384764"
                                                                                                                                                                                                                                                                                                   6020. .6101
/note="82 bp inverted repeat includes part of MTH174
(sensory transduction histidine kinase - paralog.fam. 1);
79% ID to interval 3058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="82 bp inverted repeat includes part of MTH174 (Sensory transduction histidine kinase - paralog.fam. 1); 79% ID to interval 3057" complement(6020..6082)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="63 bp direct repeat includes part of MTH174 (sensory transduction histidine kinase - paralog.fam. 1); 86% ID to interval 554696"
                                                                                                 of MTH174 paralog.fam. 1);
                  - paralog.fam. 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                 /note="72 bp direct repeat includes part
generory transduction histidine kinase -
86% ID to interval 898474"
complement(6015. .6082)
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/protein_id="AAB84682.1"
/db_xref="G1:2621219"
(sensory transduction histidine kinase 86% ID to interval 4086" complement(6011. 6082)
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Pred. No. 0.0095;
0; Mismatches 6
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/protein_id="AAB84681.1"
/db_xref="GI:2621218"
                                                                                                                                                                                                                                                                                                                                                                                                                            complement(6020. .6101)
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8114. .10111
/gene="MTH176"
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/gene="MTH175"
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/gene="MTH175"
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Best Local Simi
Matches 85;
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DWGRRYIKLAAEGSMKEMQDAVQREFEVKSRNIQQQIDILRDAAKARREDRINRLKEA
YQIAESLKLENPPLIGGQMDQQLSSIMEGALMYMRGTKALRAEIRALEERTSDDPFIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NELAITENKLEIDTESVLQAAGTKWNFLPFRPGLVGGHCIGVDPYLTHKAQSIGYHP
EILAGRRAINGGMGAYVSQLYKAMIRKIHVDGARVLVMGLTFKENCPDLRNTKVVD
IVRELAEVALAVDVYDPWVSVEEAQHEYGLTPISAPVEGNYDAVVLAVAHNEFKELGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGYAGILDLGIGRAVTOKLSSIRGSDEEMNSYTIMSTAIRTAIVGGLGFSLIIIFG
LLGGGEFFSHKDVSSLELEFSVLLLAFALPLQAISATYRGVNEAYLNFKGINLLRIFL
GATNFGGPFLVSFYAKDLHYLVTTLVLSRALAFFIFRRLAHGVLKETLVGRSCKYDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAVELFREGGWYTVSSIINPELVQSDRFFIGVLLSAAAVTSYVIPYEITIQSMILVGA
VSTVAFPSISNLIRTSFAEALECFNKWLLRYLLIMGGGMLCLAFLLPFILKLWYGDYI
GDDSISVGRILCLGVFFNALGAMFYSFLHANAKVKETAILHSIELPIFILLIILIPR
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VLDIFFVFGNYLFSYNPVYESMAAMYGDAAVVDNAGRYIKFTLPNVSSLIFLIPYVVS
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VLVETVEMGGFLIFYNTYPEYEWILFLSISWESDNSDNLERRYQFEALMGYYQDP
FGMGAGAIADYINSEEMPWAYELFYVSLYOFGILGFLFYALGYLFLLVFLXVRXI
GRRSFEFCYLSGMLAFLMATATNPYLARFDYWWVIFIPVALLNYSGANGSKSNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPRSIADPITTNSVNISGFLNILVASKEAGVKSLTYAASSSTYGDHPGLPKVEEVIGK
LEPPPAVEKVNELLADVFSRKYGENILIGLRFFRYFGKRODDNGAXAVTPKNISAMI
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                                                                                                                                                                  ALRNIQEKQAMYSTLKLDVNKVAVFRQDGVAEVPDDPVRPKKGILLVLGALSGLVMGV
MIAFIVMAVRRSRAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSTIKKVTSGSTPEVAEIVDSLYREIITAGTHKAESIKVAEAAKVIENTQRDLNIALI
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/note="ORE_7; similar to Polysaccharide biosynthesis
protein; potential multiple membrane spanning domains."
                                                                                                                                                                                                                         2303. .3568
/note="ORF_5; similar to UDP-glucose/GDP-mannose
dehydrogenase"
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/note="ORF_9; similar to Glycosyl transferase"
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epimerase/dehydratase family"
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                                     426 ATAACGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raymond, C.K., Sims, E.H., Kas, A., Spencer, D.H., Kutyavin, T.V., Trey, K.G., Zhou, Y., Kaul, R., Clendinning, J.B. and Olson, M.V. Direct Submission
Submission
Submitted (04-APR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98105-2145, USA
On May 13, 2002 this sequence version replaced gi:17975252.
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/note="ORF_4; wzz; similar to chain length determinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Agayonod. C.K., Sims, E.H., Kas, A., Spencer, D.H., Kutyavin, T.V.

Ivey, R.G., Zhou, Y., Kaul, R., Clendenning, J.B. and Olson, M.V.

Genetic variation at the O-antigen biosynthetic locus in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF_1; C-terminal coding region of rpsA"

    13401
    Organism-Pseudomonas aeruginosa"
/serotype="013"
    Ab_xref="taxon:287"

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/codon_start=1
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J. Bacteriol. 184 (13), 3614-3622 (2002)
                                                                                                     GGVLSGMWLRLIGSVSKGHLPVRREAMK
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AF498404/c
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VERSION
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AUTHORS
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JOURNAL
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PUBMED
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SOURCE
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53

10224 GCCACTGCGTCACGAACTGGCACCAGCAGGCGGTTCTATCCGCTTCGATAGCGTCCGG 10165

GCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGG

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465 ATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCG

405 ATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACC

464

404

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ACGVPVVASPVQVNIEIVENNESGLLAEGNRGWRESLQNLLQSSELRRECGRNRSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MTGATGFVGAALVESFWSSEKYRVWAGYRRESSPWPEGYTPLFL
GELGSSVAWFTESLIDTVIHGAARVHYMSETVSDPLAEFRKANVOGTLDLARQAASLG
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11334. 11374. 11374. |
//note--ORF-13; similar to Glycosyl transferase group 4;
potential multiple membrane spanning domains."
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SYSBAVCYGLGAVLLYVVSGYGSNNASQGIWLSALLASAVTGFLFWNFPPARIFMGDA
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HAYQYASRYYGRHLFYYLLAVGCINLVWLLPLALFVASGRIDGMLALLIGYLPVALAL
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STAOAFHAGGGASRQIKARRLFYSLRSRLIYIFKNLPTVSAFLILLSSLFFEFVIRSM
FSWVKLSFPALRETWSAYLMLYRWLPKWIFFNATR"
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9611. 10378
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/note="ORF_14; similar to N terminal coding region
Polysaccharide biosynthesis protein WpbM"
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0.0099;
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Best Local Similarity 49.6
Matches 118; Conservative
                                                                                                                                                                   CDS
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10284 GCCCCCATCTTCTTCCGCAGCTCCGGAGATTCGACAAGACGCTGAATGGCGTCAGCCAAC 10225

GCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAGTGCGCCCGGTCCAT 344

285

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Pred. No. 0.0099; 0; Mismatches 120; Indels

Gaps

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YAVVPEARAVAHKPRILISEIQAAALDIAVITAHRALGIRKOLDIATUSTAKUTJIHGA
AGGVGHLAIQLARRAGAQVATTISSPAKAQFTEALGATLAINYTTUWVQAVLDWTGG
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LIP*
                                                                                                                                           AP005369 300600 bp DNA Linear BCT 17-AUG-2002
Thermosynechococcus elongatus BP-1 DNA, complete genome, section
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10104 TTGGGAAGTCCTTCGCGATACGAAGGCAAGACTATATGCGAATGAGCGAAGACG 10047
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Submitted (05-JUN-2002) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; 2-6-7
Razusa kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp/cyano/Thermo/,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
Location/Qualifiers
1. 300600
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                                                                                                                                                                                                                                                                                                 Thermosynechococcus elongatus BP-1 (strain:BP-1) DNA.
Thermosynechococcus elongatus BP-1
Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
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DNA Res. (2002) In press
2 (bases 1 to 300600)
Kaneko, T.
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                                                                                              RESULT 42
AP005369/c
                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                         ORGANISM
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JOURNAL
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KEYWORDS
SOURCE
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IPERIEAVIARIDLIQWEDROCGTYSGGIRKREDLAAGILHOPOVLVIDEPTVGLDIE
SROYTWDVIARDLKAQGITIILTSHYLEEVDLASDRIVILDROKRVIASGSBEELKANIG
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TLGGIVARGILGPQAEAAGIRAGSRWSRHLDRQQSNTAAKEKKV"
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                                                                                                                                                                                                                                                                    ANAYQQAVLRGEYCPSVDIFIPTYNEPPYILRRTIVACQAIHYRNKSIYVLDDGRRSE
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OLGLOKTVLPVGHIRQLRKADLKLNDYLPHIEVDPETYEVRADGELLTCEPATVLPLA
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/gene="tl10007"
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                                                                     AE000469 10940 bp DNA linear BCT 01-DEC-2000
Escherichia coli K12 MG1655 section 359 of 400 of the complete
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Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
Mau,B. and Shao,Y.
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This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by
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Submitted (16-Jahr-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Escherichia.
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                                             CAGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTT
                                                                                                                                    389 CTGAATGA----CATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGAC
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Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with C site Nos. 'unique ID nos. for the genes in the E. coli Genetic Stock Center (GGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database; is accessible (http://cgsc.biology.yale.edu]. Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data Comments to the authors are appreciated. Updated information will be available at the E. coli Gttp://www.genetics.updated; this is sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley: added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonymm instead of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the pagence of the
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/product="PTS system, fructose-like enzyme II component"
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/translation="MTKIIAVTACPSGVAHTYMAAEALESAAKAKGWEVKVETQGSIG
LENELTAEDVASADMVILTKDIGIKFEERFAGKTIVRVNISDAVKRADAIMSKIEAHL
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/note="0359; 100 pct identical amino acid sequence and
equal length to PTWC_ECOLI SW: P32672"
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/protein_id="AAC76932.1"
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    /organism-"Escherichia coli K12"

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/gene="frwB"
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/gene="frwB"
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/note="factor Sigma70; predicted +1 start at 4141443"

us-09-674-277-2.rge

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Continuation (20 of 28) of LMFLCHR32 from base 1900001 (AL499622 Leishmania major chr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94417 TGCTGCGGATGCCGCCGACCGCCGCCCGATCACCGGTACGCCGCAGGCCATCGCCTCGA 94476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCAGTGCGGCCGGATCGTTGGGCGGCACCAGGTAGCCGGTGCGGCCGTTCAGCACGG 94416
                /db_xref="G1:1790390"
/translation="MAYLVAVTACVSGVAHTYMAAERLEKLCLLEKWGVSIETQGALG
TENRLADEDIRRADVALLITDIELAGAERFEHCRYVQCSIYAFLREPQRVMSAVRVL
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                                                                                                                                                                                                                                                                                                70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 CATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAG
                                                                                                                                                                                                                                                                                                11 TGGAAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAGTAGGCC
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                                                                                                                                                                                                                  Length 10940;
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                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                    Score 45.4; DB 1;
Pred. No. 0.015;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45.4; DB 2;
Pred. No. 0.025;
0; Mismatches 101;
/protein_id="AAC76935.1"
                                                                                                                                                        complement(5234. .6085)
/gene="yijo"
                                                                                                complement(5234. .6085)
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                                                                                                                     /gene="yijo"
/note="b3954"
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                                                                                SAPQQTHLILE"
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Local Similarity 51.2%;
hes 106; Conservative
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2700001
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Best Local Similarity
Matches 70; Conserv
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LMFLCHR32_01
LMFLCHR32_03
LMFLCHR32_04
LMFLCHR32_04
LMFLCHR32_05
LMFLCHR32_06
LMFLCHR32_06
LMFLCHR32_06
LMFLCHR32_08
LMFLCHR32_09
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LMFLCHR32_14
LMFLCHR32_15
LMFLCHR32_16
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LMFLCHR32_19
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LMFLCHR32_11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 44
LMFLCHR32_19
WPCOMMENT
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KGCPHLCPWCANPESISGKIQTVRREAKCLHCAKCLRDADECPSGAFERIGRDISLDA
LEREWMKDDIFFRTSGGGYTLSGGEYLMQAEFATRFLQRLRWGVSCAIETAGDAPAS
KLLPLAKLDEVLEDVLFDLKIMDATQARDVVKMNLPRYLENLRLLVSEGVNVIPRLPLIPG
FTLSRENMQOALDVIPLNIRQIHLLPFHQYGEPKYRLLGKTWSMKEVPAPSSADVAT
MREMAERAGLQYTVGG"
                                                                                                                                                                                                                                                                                                                                                        KATAY ILEHYEISINDEELIAGNRIYKPRAGIMSPENDPYMLIKELDOPPTRPQDRFA
ISEEDRRIYREELPYWEKSMKDFINGOWIDEVKAATNIOTESINOTDKGGHIIID
YPRIJNHGIGELVAOMOQHOQOPENHFYQAALLILERSOKHILKYRAELAETWAANCT
DAGRREELITIAELSHNAOHPYPEWQACOLEWYNNIILOYESNASSIJSIGFBOYN
LPFYQTSLIQGEDAAFLKELLESLWYKONDIYLLKSTSSARYFAGFPTGYTALLGGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGSVVGATPDCRFRAGEQLADGGLSPMLGQDAQCPTAVIKSVSKLDNTLLSNGTLLNVK
FTPATLEGEAGLRKLADFLRAFTQLKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVA
GYSAFFVELSKEIQDDIIRRTRHQL"
3129.
//note="REP" (repetitive extragenic palindromic) element;
contains 1 REP sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGRSAVNVISFLCLDAYQSVQLPQPNLGVRTNALIDTPFLMKTAETIRFGTGIPQIF
NDEVVVPAFIJNRGVSLEDARDYSVVGCVELSIPGRTYGLHDIAMFNLLKVMEICLHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DITDGGARYNFSGVQGIGIANLSDSLHALKGMVFEQQRLSFDELLSVLKANFATPEGE
                                                                                                                                                                                                                                                                                                                                          /translation-"MTNRISRLKTALFANTREISLERALLYTASHRQTEGEPVILRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGNAALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPVPLLSSFISDCLEKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVRARLINRFEKYGNDIDEVDNISAELLRHYCKEVEKYQNPRGGYFTPGSYTVSAHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="enzyme; Degradation of small molecules: Carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 pct identical to PFLC_ECOLI SW: P32675"
                                                                                                                                                            'function="enzyme; Energy metabolism, carbon: Anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="0113; 100 pct identical amino acid sequence and equal length to PTWX_ECOLI SW: P32676"
                                                                                                                                                                                               /note="0765; 100 pct identical amino acid sequence and equal length to PFLD_ECOLI SW: P32674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="putative enzyme; Energy metabolism, carbon:
Anaerobic respiration"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"factor Sigma70; predicted +1 start at 4144712"
1906. .5247
                      Sigma70; predicted +1 start at 4141533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="factor Sigma70; predicted +1 start at 4144578'
1864. .4894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="probable pyruvate formate lyase activating enzyme 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
/product="PTS system fructose-like IIB component 2"
                                                                                                                                                                                                                                                                            /product="formate acetyltransferase 2"
/protein_id="AAC76933.1"
/db_xref="G1:1790388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAC76934.1"
/db_xref="G1:1790389"
                                                                                                                                        EC_number="2.3.1.54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EC_number-"1.97.1.4"
                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                           /codon_start=1
                      factor
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/gene="pflC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="b3953"
                                                                              note="b3951"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1730. .4760
/gene="pflc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4026. .4904
/gene="pflC"
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gene="frwD"
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/gene="pflc"
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misc_difference
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94477 CCGGCGTGATGCCGAACGCTCGTACCATGGCGTGGTGACGAACACATCGGCCGCGCTGT 94536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-SEP-1993) 608-263-7459
Submitted (03-SEP-1993) 608-263-7459
Submitted (03-SEP-1993) 608-263-7459
Submitted (03-SEP-1993) 608-263-7459
This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Misconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps and conflicts with other sequence determinations are annotated. The start of this entry overlaps the end of the entry ECOWWR (L19201) by 93 bp. NOTE: An update was submitted on 25-OCT-1993, reflecting a correction to the hemE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sub_strain="MG1655"
/db_xref="taxon:562"
/db_xref="taxon:562"
/note="This sequence comprises the following lambda
/note="This sequence comprises the following lambda
/note="This sequence comprises the following lambda
/note="This sequence comprises the following lambda
/note="This sequence comprises the following"
/note="This sequence comprises the following lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lambda lamb
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DITULAGVVOEKAASAAGLESIHVPPRPRFRVDARQDOTDIEBEELLEBTADGFRNYRA
RLDVSTFESLLIDRAQOLILIAPPEWTALVGGRRVLGANFDGSRNGVFTDRVGTLSNDF
FVNLLDMRYEWKATDESKELFPGRDRETGEVKFTASRADLVFGSNSVLRAVARSY
                                                                                                                                                                                                                                                                                                                                                                                                            BCT 17-DEC-1993
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/note="CG Site No. 14983"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli (sub_strain MG1655, strain K-12) (library: lambda)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation" "AITSGLEVVWTQTPTQWSNYFFENLFRYEWVQTRSPAGAIQFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDAPELIPDPFDPSKKRKPTMLVTDLTLRFDPEFEKISRRFLNDPQAFNEAFAXWFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTHRDMGPKSRYIGPEVPKEDLIWQDPLPQPIYNPTEQDIIDLKFAIADSGLSVSELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes
Nucleic Acids Res. 21 (23), 5408-5417 (1993)
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 176195)
Blattner,F.R., Burland,V., Plunkett,G. III, Sofia,H.J. and
                                                                                                                                                                                                                                                                                                                                                                                              ECOUW89 176195 bp DNA linear BC E. coli chromosomal region from 89.2 to 92.8 minutes. U00006
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protein_id="AAC43048.1"
db_xref="GI:396289"
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                                                                                                                                                                       94537 AGAACAGCCGCAGCTGGTCACGGCCGC 94563
                                                                                        517 AGACCGGTAACGCTGGGAAAAGGGCAC 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .176195
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Blattner, F.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U00006.1 GI:409785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels, D.L.
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ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
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AUTHORS
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AUTHORS
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SYIGAFDFTALKCIFGALVLFIVLLIRGRGWRPTPFKYTLAIALLOTGGWGTAGWYY
VSGGAGKVALLSYMPFWVYIFAALFLGERLRRGGYFAILIAAFGLFLVLQPWQLDFS
SWKSAMLAILSGSWGGASTVARKLYSKRHPRVDLLSITSWQMIYAALVWSVYALLYPQ
REIDWQPTVFWALAY SAILAYLAMSLWLFYLKNLPASIASLSTLAVPVCGVLFSWWL
LGENPGAVEGSGIVLIVLALALVSRKKKEAVSVKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=ORF_f205
//potean_id="AaC43050.1"
//potean_id="AaC43050.1"
//db_xref="f1:305091"
//translation="MKASLALLSLITAFTSHSLKSPAVPPTVVQIQANTNLAIADGAR
//translation="MKASLALLSLITAFTSHSLKSPAVPPTVVQIQANTNLAIADGAR
GOGSTLFYDPAYVOLTYPGGDYPORRGVCSDYVIRALRSGRVDLOKLVHEDMAKNPA
EYPGWKKKRPDSNIDHRYPVPNLETWFSRHDKTRPTSKNPSDYQAGDIVSWRLDNGLA
HIGVVSDGFARADGTPLVIHNIGAGAQEEDVLFNWRWVGHYRYFVK"
complement(2886. .2915)
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WLVVGDKFYLAGFAQSTVEKSFKDAGILVVEIAFFGGESSQNETDBLRGTAETAQCGAIL
GIGGGTLDTARALAHFWGVPVAIAPTASTDAPCSALSVIYTDBGEFDRYLLLDNNP
NWYIVDTKIVAGAPARLLAAGIGDALATWFERACSRSGATTWAGGKCTQAALALAEL
CYNTLLEEGEKAMLAAEQHVVTPALERVIEANTYLSGVGFESGGLAAAHAVHNGLTAI
BADHYYYGREKVAFGTLTQLVJENAPVERIETYAALSHAVGLPITLAQLDIREDVPAK
MRIVARAACAEGETIHNMFGGATPDQVYAALLAVADOYGGRFLQEWE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MGERKLHTGSLMSAAGKSNPLAISGLVVLTLIWSYSWIFMKOVT
                                                                                                                                                                                                                                                                                                                                                                                                                             1317. 2255
/note-"similar to Desulfurolobus ambivalens hypoth. 28.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="promoter matrix score of 42; putative; within ORF f205, which would suggest alternate start codon" 2912. .3053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted bend of 81 degrees"
3031. 3064
/standard_name="REP; repetitive extragenic palindromic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="gldA" /note="similar to Bacillus stearothermophilus glycerol dehydrogenase"
                                                                                                                                                                                /note="93 bp overlap with end of L19201 (ECOWU87)"
156. .15760
                                                                                      'note" corresponds to lambda clone EC18-126"
                                                                                                                                                                                                                                         'note="corresponds to lambda clone EC14-54"
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/protein_id="AAC43051.1"
/db_xref="G1:396292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1429. .1432
/note="TTT in M21516; TTTT here"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kDa protein in sor 3' region"
                                                                                                                                                                                                                                                                                                                                /note="G in M21516; C here"
1266: .1305
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DAHEKFVKDFVAAWVKVMNLDRFDLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC43049.1"
/db_xref="GI:409786"
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/gene="gldA"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                   'note="putative"
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/label=ORF_f380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=0RF_0312
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    .93
    /qene="katG"

                                                      'gene="katG"
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CDS

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Consensus quality: 168540 bases at least Q40
Consensus quality: 179014 bases at least Q30
Consensus quality: 179014 bases at least Q30
Consensus quality: 181723 bases at least Q30
Consensus quality: 181723 bases at least Q30
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 192846; sum-of-contigs estimation
Quality coverage: 7.8 in Q20 bases; agarose-fp estimation

* NOTE: This is a "working draft' sequence. It currently

* consists of 34 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                     AC023609 196146 bp DNA linear HTG 29-JUN-2000
Mus musculus clone CT7-405C9, WORKING DRAFT SEQUENCE, 34 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 196146)

DOE Joint Genome Institute.

Direct Submission

Submitted (16-FEB-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

on Jun 29, 2000 this sequence version replaced 91:6980219.
                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
gap of unknown length
contig of 1184 bp in length
gap of unknown length
contig of 1329 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 1195 bp in length
gap of unknown length
contig of 1136 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1058 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown length
of 1050 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center Project Name: 1108758
Center clone name: RG-MBAC_405C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.jgi.doe.gov
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Center Code: JGI
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 196146)
DOE Joint Genome Institute.
Sequencing of Mouse
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AC023609.2 GI:8810275
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AUTHORS
TITLE
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                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
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/protein_id="AAC43055.1"
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/translation="WNELVOILKNTROHLMTGVSHMIPFVVSGGILLAVSVMLYGKGA
/translation="WNELVOILKNTROHLAMYGYSHMIPFVVSGGILLAVSVMLYGKGA"
VPDAVADPNIKKLFDIGVAGITLMVPFLAAYIGYSIAERSALAPCAIGAWVGNSFGAG
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LINSLIQWLQGMQQGSIVMLAVIMGLMLAFDWGGPVNKVAXAFWLICVAQGVTTVVAI
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LKNIEFRILDSDGATSAILEAHRSIAGDTSLREHILAGVSAGISCAERIVASANHFCE
ERSESSSYLQERALDVCFQLLQQTYGEQREPPOGKLTQPAICMADELIPSOFLE
LDKNHLKGLLLKSGCTTSHTVILARSFNIPTLVGVDIDALTPWQQOTXIDGNAGAIV
VEPGERAVRYYQQEARVQDALREQORVWLTQQARTADGIRIEIAANIAHSVEAQAAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGAEGVGLERTEMLYMDRTSAPGESELYNIFCQALESANGRSIIVRTMDIGGDKPVDY
LNIPAEANPFLGYRAVRIYEEYASLFTTQLRSILRASAHGSLKIMIPMISSMEEILWV
KEKLAEAKQQLRNEHIPFDEKIQLGIMLEVPSVWFIIDQCCEEIDFFSIGSNDLTQYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAVDRDNAKTTRHYNSLNPAFLRALDYAVQAVHROGKWIGLCGELGAKGSVLPLLVGL
GLDELSMSAPSIPAAKARMAQLDSRECRKLLNOAMACRTSLEVEHLLAOFRWTQQDAP
LVTAECITLESDWRSKEEVLKGMTDNI.LLAGRCRYPRKLEADLWAREAVFSTGLGFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIPHSKSEHIEQSTISVARLQAPVRWGDDEAQFIIMLTLNKHAAGDQHWRIFSRLARR
IMHEEFRNALVNAASADAIASLLQHELEL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WCASCSSAPEISNWQLSPASVSVPISARALLALPCGQCAGYATQFVMKKYYTAFQRGL
                                                                                                                                                                                                                                    RLOKA IGDEGILFAQTMSRDAQGMYEBAKRLRDA IPGIVVKIPVTSEGLAAIKILKKE
GITTLGTAVYSAAQGLLAALAGAKYVAPYVNRVDAQGGDGIRTVQELQTLLEMHAPES
MVLAASFKTPRQALDCLLAGCESITLPLDVAQQMLNTPAVESAIEKFEHDWNAAFGTT
                                                                                                                                                                                           /db_xref="GI:396293"
/translation="MELYLDTANVAEVERLARIFPIAGYTTNPSIIAASKESIWEVLP
                                                                                                                                                                                                                                                                                                                              complement(4922. .4949)
/note="promoter matrix score of 47; putative; within ORF f220, which would suggest alternate start codon"
complement(4962. .7097)
/note="similar to phosphotransferase system enzyme I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="putative"
7771. 8850
/note="similar to phosphotransferase system enzyme II"
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                                   complement(4288. .4950)
/note="similar to Bacillus subtills hypoth. 20 kDa
protein, in tsr 3' region"
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note="promoter matrix score of 46; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7200. .25839
/note="corresponds to lambda clone EC21-52"
7578. .7699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.4; DB 1; Leuy... -
Pred. No. 0.027;
           'note="predicted bend of 75 degrees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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/db_xref="GI:409788"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=ORF_f711
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                                                                                                                                                                      'protein_id="AAC43052.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="GI:409787
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/transl_table=11
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                                                                                                                             'transl_table=11
                                                                                                                                                        /label=0RF_f220
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Matches 70;
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CDS

CDS

bp in length length

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· 71 TGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAATGT 121

11 TGGAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAGTAGGCC 70

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contig gap of

14174:

length

unknown

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 254993)
Montgomery, K.T., Grills, G., Han, J., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., High Throughput Mouse Sequencing
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-AUG-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA On Jan 26, 2002 this sequence version replaced gi:14488282.
                                                                                                                                                                                                                                                                                                                                                                                                                                          2. (bases 1 to 254993)
Montgomery,K.T., Grills,G., Han,J., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Rucherlapati,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: agarose-FP - N/A Quality coverage: 6 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Contact: http://www.hpcgg.org/Sequence/mouse.html
Contact: http://www.hpcgg.org/Sequence/mouse.html
Contact: http://www.hpcgg.org/Sequence/mouse.html
Contact: http://www.hpcgg.org/Sequence/mouse.html
Contact: http://www.hpcgg.org/Sequence/mouse.html
Contact: http://www.hpcgg.org/Sequence/mouse.html
Sequence/ng vector: puc18; L0875
Contact: py-terminator Big pye; 100%
*Consensus quality: 245508 at least Q30
*Consensus quality: 245508 at least Q40
Extimated insert size: agarose-FP - N/A
**Estimated insert size: 254133 - sum-of-contigs
Quality coverage: agarose-FP - N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 27415 bp in length contig of 30382 bp in length gap of unknown length contig of 23800 bp in length gap of unknown length gap of unknown length contig of 20498 bp in length gap of unknown length contig of 19025 bp in length gap of unknown length contig of 1883 bp in length gap of unknown length contig of 13853 bp in length gap of unknown length contig of 21595 bp in length gap of unknown length gap of unknown length contig of 21593 bp in length gap of unknown length gap of unknown length contig of 12593 bp in length gap of unknown length contig of 8429 bp in length gap of unknown length gap of unknown length contig of 5225 bp in length gap of unknown length contig of 5225 bp in length gap of unknown length
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of 5870 bp in length
AC078885.8 GI:18376842
HTG; HTGS_PHASE1; HTGS_DRAFT.
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/strain="C57BL6/J"
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125020 bp DNA linear PRI 18-JAN-2002
AP429315.1 GI:17646244
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3.8%; Score 45.4; DB 2; Length 254993;
Best Local Similarity 63.1%; Pred. No. 0.03;
Matches 70; Conservative 0; Mismatches 41; Indels 0;
                                                                                                             //octe="assembly_name:Contiglia" / note="assembly_name:Contiglia" / 12120. / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Contiglia" / note="assembly_name:Co
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/note="assembly_name:Contigl36"
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Homo sapiens. Homo sapiens

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/protein_id="AAM27622.1"
/db_xref="G1:20559851"
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/note="ORF_2; himD/lhfB"
/codon_start=1
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/protein_id="AAM27624.1"
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/db_xref="taxon:287"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTCCCCGTATTTAAACAATGTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 GGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGAC 397
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L. aspeate expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
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                                                                                                                                                                               2 (bases 1 to 125020)
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
Submitted (05-007-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCGGGCTGAAAAGAGGATCCGCCGTTATCTGTTGCATTTC-CCCTTAGCCTGACTAGC
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                                                                                                                                                                                                                                                                                                                                               /map="16924.3; between D168520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
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llarity 13.5%; Pred. No. 0.04;
Conservative 237; Mismatches 279; Indels 1;
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/gene="JPH3"
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/gene="JPH3"
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complement(<36507. .36887)
/gene="JPH3"
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                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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17736 WKRSGSMISSCYYYSASSCMWHMSSKSCMCCCMMMKRRCACCYSSMSCTSMYRCCWGGMK 17795
                                                                                              Pseudomonas aeruginosa serotype 014 putative O-antigen biosynthesis gene cluster, partial sequence.
AF498405 AC104724
AF498405.1 GI:20559850
17616 MIYMCCCWRRRSYMYYRSMSAMGMRKSSWSGMRMMGSASSRRCKSASRSSWCSRRMKGMR 17675
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IRGFGSFSLHYRAPRVGRNPKTGESVRLDGKFVPHFKPGKELRDRVNEPE"
                                                                                                                                                                                       458 CAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTA 517
                                                                                                                                                                                                                                                                                                             GACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGGCTCATTCCCCAGGTG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578 TICTGTCTGCTGACGCAGACGTGCTTCGTATTCTTCACGCCCGGCGCCCACCACGAGC 635
                                                          398 ATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGC
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Raymond, C.K., Sims, E.H., Kas, A., Spencer, D.H., Kutyavin, T.V., Ivey, R.G., Zhou, Y., Kaul, R., Clendenning, J.B. and Olson, M.V. Genetic variation at the O-antigen blosynthetic locus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 13413)
Raymond, C.K., Sims, E.H., Kas, A., Spencer, D.H., Kutyavin, T.V., Ivey, R.G., Zhou, Y., Kaul, R., Clendinning, J.B. and Olson, M.V. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-ARR-2002) Genome Center, University of Washin Box 352145, Seattle, WA 98105-2145, USA On May 13, 2002 this sequence version replaced gi:17975253. Location/Qualifiers
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/note="ORF_1; C-terminal coding region of rpsA"</pre>
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/organism="Pseudomonas aeruginosa"
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J. Bacteriol. 184 (13), 3614-3622 (2002)
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us-09-674-277-2.rge

CDS

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DMISPEGGHAWLFIAAPLVAIPLFIRECMYRAVMRYICANDALIAIAKAYTISAIVLSL
LVYMYRSPRAVVPRSLVFNYWWLSMLLIGGLRLAMRQYFMGDMYSAVQSVPFLNRQDG
LPRVAIYGAGAAGNQLVAALRLGRAMRPVAFIDDDKQIANRVIAGLRVYTAKHIRQMI
DETGAQEVLLAIPSATRARRREILESLEPFPLHVRSWPGFMDLASGRVKVDDLQEVDI
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SYBRAVCYCIGAVLLWVYSGVGSDDASOGIWLSALLASAVFRELEWFPRAFFWGDA
GSGFLGIILAGLSLQAAWVSPQLFWGWLILLGVFVVDATLTLILRELKGDKYYBAHRS
HRYQYBASRYGGHLPYTLAVGCINLVWLLPLALFVASGRIDGMLALLIGYLPVALAL
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EGLPKVLVEBAACGRVVVTTDVPGCRDAIEADRTGLLVPVRDAVALADAIQRLVESPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRRFIYLSSIKVNGEGGEPGOPYVADSLPNPVDPYGYSKLEAEDALLGLAAETGLEVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEI IPTVIDLKRYEVRDESCEKKTVIGWIGSPSTOKYILDIAPELVKLCVEYOASMLL.
VGATPEISSYFSGVYVDVKAWKEEDEVGYIROWTIGIMPLPDGPWEKGKCGYKLIQYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9610. .10377
/note="ORF_11; similar to Glycosyl transferases group 1"
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/note="ORF_13; similar to Glycosyl transferase group 4;
potential multiple membrane spanning domains."
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                                                                                                                                                                         8097. .9167
/note="ORF_10; similar to Glycosyl transferases group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 13413;
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/note-"ORF_12; similar to NAD dependent
epimerase/dehydratase family"
                                                                                                                                    FSMVKLSLPALRETWSAYLMLYRWLPKWIFFNATR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAVELFREGGWVTVSSIINPFLVQSDRFFIGVLLSAAAVTSYVIPYEITIQSMILVGA
VSTVARPSISNLIRTSFAEALECFNKWLLRVLLIMGGGMLCLAFLLPFILKLWVGDYI
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HGIVGAAVAMSLRTLADTIVLAVLSYFSGWRVKFANC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKSPIIDVVVVNWNAGLQLRSCVDSIFKNSFGLIRKVIVIDNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPRSIADPITINSVNISGFLNILVASKEAGYKSLIYAASSSTYCDHPGLPKVEEVIGK
PLSPYAVTKYVNELYADVFSRCYGFNLIGLRYFNVFGKRODPNGAXAAVIPKWISAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGEPYY INGDGETSRRFCFINNVIKANLLAAFCETEEAKNQVYNVAYGGRTTLGQLFD
SLKVELSRNGINYEQGPIYREFRAGDVRHSQAEIKKAQAYLGYNPEYDIQAGIAEAMP
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NELAIIRNKLEIDTESVLQAAGTKWNFLPFRPGLVGGHCIGVDPYYLTHKAQSIGYHP
EIILAGRRLNDGMGAYVVSQLVKAMLRKRIHVDGARVLVMGLTFKENCPDLRNIKVVD
IVRELAEXNIAVDYXDPWVSVEEAQHEYGLTPISAPVEGNYDAVVLAVAHNEFKELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDDFSTGHMYNLDEVRGLVGEERWRNFKLIQGDIRDIGDCRRAVEGVDYVLHQAALGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQIAESLKLENPPLIGGOMDOQLSSIMEGALMYMRGTKALRAEIRALEERTSDDPFIP
ALRNIQERQAMYSTIKLDVNRVAVFRQDGVAEVPDDPVRPKKGILLVLGALSGLVWGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSTLEVEKEELESAVHLKFTSTLSELQECNFFIVTVPTPIDEHKQPDLTPLVKASESI
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RNFFREVY LPSLSENERSGSKDRLY SNLSEEME LORPSKDERERY TV IF EKHDPGGAA
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                                                                                                                          1167. .2216
/note="ORF_4; wzz; similar to chain length determinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4000. .3534
foote="ORF-7; similar to Polysaccharide biosynthesis
protein; potential multiple membrane spanning domains.
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7156. .8091
/note="ORF_9; similar to Glycosyl transferase"
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June 17, 2003, 15:59:59; Search time 2683.55 Seconds (without alignments) 16148.066 Million cell updates/sec US-09-674-277-1 1489 1 ctgcagtccggagatgaaag......ttggaaggagcctggtcgac 1489 4109280 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapox 1.0 em_htgo_hum: * em_htgo_mus: * em_htgo_other: * em_un:* em_vi:* em_htg_hum:* em_htg_inv:* em_htg_other:* em_htg_pln:* em_htg_rod:* em_htg_mam:* Minimum DB seq length: 0
Maximum DB seq length: 2000000000 em_htg_vrt:* em_htg_mus:* gb_sts:* gb_sy:* gb_un:* em_fun:*em_hum:* em_ro:* em_sts:* gb_ba:*
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gb_on:*
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gb_pat:*
gb_ph:*
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gb_ph:* em_om:* em_or:* em_pat:4 em_ba:* em_in:* em_mu:* gb_vi:* em_ov:* GenEmbl:* Perfect score: Sequence: Scoring table: Database : Searched: Run on: Title:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	X68081 M. tuberculo U06266 Mycobacteri U06268 Mycobacteri U06256 Mycobacteri AL121746 Streptomy U06272 Mycobacteri U06272 Mycobacteri AB020123 Bacillus AB020123 Bacillus AB020124 Bacillus AB020125 Bacillus AB020125 Bacillus AB020156 Bacillus AB020158 Bacillus		linear PAT 06-SEP-2000	sion; Enterobacteriaceae;	nemorrhagic escheri	UE THERESE MARI (FR); LAURE DIAGNOSTICS (FR)	6; Length 1489; 0; Indels 0; Gaps 0;	CATCAGCGTGGTCCCGCAGGCCA 60 	TGAACCTICCGGTTGTTTCTCCA 120 			TCCGTGCAGCGGGCTATTTCAGG 300 	AGCTTTTGTTTCTGACATCCAC 360 	GCATCGTCAGTTGCGCTTGGAA 420
	0 1 MTKATGCP 14 1 MTU06268 14 1 MTU06268 12 1 SCF73 12 1 MTU06272 13 1 MTU06272 14 1 AB020123 14 1 AB020128 14 1 AB020128	ALIGNMENTS	1489 bp DNA from Patent W09955908. GI:9997847	ii. 11 sobacteria; gamma subdivision; 1489)	schon, D.T. and Laure, F.C. Lences for detecting enterohemorrhagic 1908-A 1 04-NOV-1999;	THIERRY DOMINIQUE (FR); FRECHON DOMINIQUE FRANCOISE CLAUDINE (FR); PASTEUR SANOFI DI LOCALLON/QUALIÍLERS 1 1489 //Organism="Escherichia coli" //db.xref="taxon:562"	c 391 g 358 t 08; Score 1489; DB 08; Pred. No. 0; Mismatches	GAAAGCACCACTGTGTGTACCC 	TGATITITGICACAGACICAATGACTACCGGACGCACTGAACCTICCGGTIGITTCICCA 	gccagttaagccagcggtttcctgctgaaaatgtcggcaaaacggggaagcatcagaa 	GGGCGGGGGGAACTCCGTCCGGCCAGTGAACCGTGCCACACTCCGGGCAGTACATGCCGCC 	GGCGCTGATACCGGCAAGAATGGTCGCAAACTCCCGCTCCGTGCAGCGGGCTATTTCAGG 	ATACCCTTCGTCATCAACACGTACAAACCAGAAGACCAGCTTTTTGTTTCTACACATCAC	aaagaaggaatatcaggtctgcgcagcactcaacggcatcgtcagttgcggcttggaa
-	296.4 19.9 4810 296.4 19.9 2308 295.8 19.9 2316 295.6 19.9 14922 295.6 19.9 2312 295.8 19.7 2208 293.8 19.7 2238 293.8 19.7 2238 293.8 19.7 2238 293.8 19.7 2238		AX011297 Sequence 1 AX011297 AX011297.1		Thierry, D., Frechon, D.T. Nucleotide sequences for coli (ehec) Patent: WO 9955908-A 1 04	Φ	386 a tch al Similari 1489; Cons	1 CTGCAGTCCGGA(61 TGATTTTGTCAC 		181 GGGCGGGGAACT 	241 GGCGCTGATACCC	301 ATACCCTTCGTC2 	361 AAAGAAGGAATI
	0 111110 101110 1011111111111111111111		RESULT 1 AX011297 LOCUS DEFINITION ACCESSION VERSION	SOURCE SOURCE ORGANISM REFERENCE	AUTHORS TITLE JOURNAL	FEATURES SOUIC	DASE COUNT ORIGIN Query Match Best Local Matches 148	QV Qu	Qy	Qy Dp	da Db	oy oy	Qy	og .
	AB020078 Bacillus AB02016 Bacillus AB020116 Bacillus AB020117 Bacillus AB020064 Bacillus AB020075 Bacillus AB020072 Bacillus AB020073 Bacillus AB020073 Bacillus AB020074 Bacillus AB020075 Bacillus AB020077 Bacillus AB020077 Bacillus AB020077 Bacillus	AB020079 Bacillus AB020080 Bacillus AB020081 Bacillus AB020081 Bacillus	AB020082 Bacillus AB020084 Bacillus AB020085 Bacillus AB020085 Bacillus AB020086 Bacillus AB020086 Bacillus AB020087 Bacillus	AB020090 Bacillus AB020093 Bacillus AB020095 Bacillus AB020097 Bacillus AB020097 Bacillus AB020098 Bacillus	AB020099 Bacillus AB020101 Bacillus AB020102 Bacillus AB020104 Bacillus	AB020105 Bacillus AB020107 Bacillus AB020108 Bacillus AB020109 Bacillus AB020110 Bacillus AB020111 Bacillus	AB020112 Bacillus AB020113 Bacillus AB020114 Bacillus AB020116 Bacillus AB020066 Bacillus AB020070 Bacillus	AB020089 Bacillus AB020095 Bacillus AB020100 Bacillus AB02011 Bacillus AB020121 Bacillus	AB02019 Bacillus AB020103 Bacillus AB020103 Bacillus M29876 B.stearothe AF314107 Mycobacte	AF114108 Mycobacte AF314109 Mycobacte AF314110 Mycobacte AF314112 Mycobacte	AF314113 Mycobacte AF314114 Mycobacte AF314116 Mycobacte AF314118 Mycobacte	AF314119 Mycobacte AF314122 Mycobacte AF314124 Mycobacte X83777 M howis kat	U41307 Mycobacteri U41308 Mycobacteri U41309 Mycobacteri U41311 Mycobacteri	U41312 Mycobacteri AF314123 Mycobacte U06259 Mycobacteri
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Burland, V., Shao, Y., Perna, N.T., Plunkett, G. III, Sofia, H.J. and
Blattner, F.R.
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                                                                                                           subdivision; Enterobacteriaceae;
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P33693"
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SW:
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The complete DNA sequence and analysis of the plasmid of Escherichia coll 0157:H7
98391744
                                                                                                                                           Shao, Y., Perna, N.T., Plunkett, G.,
                                                                                                                                                                                                                                                                                                                          coli 0157:H7"
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approx. 269 aa protein EXOK_RHIME S
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Submitted (25-JUN-1998) Genetics, Uni
Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
1. 9207
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                                                                                                              gamma
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Escherichia.
                                                                                  Escherichia coli O157:H7
Escherichia coli O157:H7
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Burland, V., Shao, Y.,
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AUTHORS
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3032. 3035
/note="100 pct identical (0 gaps) to RBS at 641. 644 locus ECNRIRE accession x02302"
3040. 3897
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4072. 4080
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segment for replication of E. coli IncFII plasmid NR1
ECREPAI X12776"
                                             /note="91 pct identical (0 gaps) to 24 residues of an approx. 24 aa protein uORF P30REPFIC, accession M16167, translationally coupled to replication initiation protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="replication initiation protein"
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SEDAVAAARRSKVEWENRIRKKQGLDTLGMDELIAKAWRFVRERFRSYQTELKSRGIK
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length to REP2_ECOLI SW: P03066"
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Pred. No. 0;
0; Mismatches
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99.9%; Pred
0; )
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                                                                                                                                    /translation="MRKYIPLVLFIFSWPVLCADIHGRYVRVLDGDTIEVMDSRKAVR
IRLVNIDAPEKKQDYGRWSTDMMKSLVAGKTVTYTYFQRDRYGRWLGQVYAPDGMNVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="d1:3822118"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1905. .2243
/gene="L7005"
/note="98 pct identical (0 gaps) to 57 residues of an
approx. 200 as protein; plasmid R100 miniplasmid pSM1 ORF
4, TRSW: Q52340"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKLITFILIVLIIAALLIRIILRSVNQHSPLLMQLHAAGIRTGD
AERILSGGEYDASHLRPERRRRDILLEEVLRQAGIPLLRSHDARKLLQMTGEWLNTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="initiation site; Escherichia coli plasmid R100 ssiB
gene; 99 pct identical to ssiB locus R108SIB accession
D90185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSQTENAVTSSSGAKRAYRKGNPLSDAEKQRLSVARKRASFKEV
KVFLEPRYKAMLMQMCHEDGLTQAEVLTALIKSEAQKRCV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7416. .2421
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2439. .2445
/note="100 pct identical (0 gaps) to the -10 region at 46. .52 locus ECNRIREP accession X02302"
/note="100 pct identical (0 gaps) to RBS at 80. .85 locus ECNRIREP accession X02302"
                                             /product="hypothetical protein 15.6 kDa protein in fin0 3'
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length to CPB2_ECOLI SW: P03847"
                                                                                                                                                                                                                                                                                                                                              note="55 pct identical (0 gaps) to 66 residues of ipprox. 72 aa protein HHA_ECOLI SW: P23870"
                                                                                                                                                                                                                                                                                                                                                                                                                                          product "putative hemolysin expression modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 899. .1927
note="predicted sigma 70 promoter; score of 56%"
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2973. .3047
                                                                                                                                                                                                                                note-"predicted sigma 70 promoter; score of 56%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="CopB protein (RepA2 protein)"
/protein_id="AAC70074.1"
/db_xref="GI:3822120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="hypothetical protein"
protein_id="AAC70073.1"
db_xref="G1:3822119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHRLAELITGKLYDRIPKEIWKYVR
                                                                     region precursor"
/protein_id="AAC70071.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAC70072.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2240. .2327)
                                                                                                                 db_xref="GI:382211"
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/transl_table=11
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'trans1_table=11
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'gene="L7005"
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'gene="L7004"
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gene="L7004"
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gene="cpb2"
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39 1200 ACGGGAAGCATTTTGCGTATGCCCATGGCCA 075 075 07 1320 GGAGGGCATACTTTGCGTATGGCCATG 99 150 GGAGGGCATACATTTGGTAAAGCACATG 135 GGAGGGCATACATTTGGTAAAGCACATG 135	29 1380 GGGCCTGATGGTGCACCTGTGGAGGAGC 59 Db 8216 GGGCCTGATGGTCCACTTGGAGGAGC 195 Qy 1440 GGAAACGGCAAATATACCATCACCAGTG 19 Db 8276 GGAAACGCCAATATACCATCACCAGTG 255	RESULT 3	Escherichia. REFERENCE 1 (bases 1 to 92077) AUTHORS IVERSEA,P.L. TITLE Antisense antibacterial JOURNAL Patent: WO 0149775-A 9 Avi Biopharma, Inc. (US FEATURES Location/Quali	/organism="Ec /db_xref="tax BASE COUNT 24693 a 20133 c 2: ORIGIN	Ouery Match Best Local 8 Matches 1488	9 DD 6836 CTGCAGTCCGAGATGAACAGCACCACT 35 QY 60 ATGATTTTGTCACAGACTCAATGACTAC 9 DD 6896 ATGATTTTGTCACAATGACTA 95 6896 ATGATTTTGTCACAATGACTA	9 0y 120 5 Db 6956	9 C7 C9 C9 C9 C9 C9 C9 C9 C9 C9 C9 C9 C9 C9	9 0y 300 5 0v 360	9 Db 7
SGTCGGCCGGTGAACCGTGCCACACTCCGGGCAGTACATGCCGC	- w r 4 i	TGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATC 4	ATAAAAAAACTCTTCCTGTTCTGATTCTTGGGGGGGGGG	7		TGGCACGGTCCCGGAACATACAGGACATATGATGCCGGGGGGGG		CTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGA 107 L		1200 ATTTATGTCAATCCTGAAGGCCCGGTGGAAACCAGATCCTCTGGCTTCCGCGAAAGAT 125
A AGGCGGGGGAACTCC	300 7136 360 7196	Oy 420 ACCCTTAGTATTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7376 600 7436 660	Db 7496 CCTCTGAGATT Qy 720 AGATTTCAACA	780	Oy 840 TGGCACGGTGC Db 7676 TGGCACGGTGC Oy 900 CAACGTTTGA Db 7736 CAACGTTTTGA		Oy 1020 CTGACTGGTAA Db 7856 CTGACTGGTAA Oy 1080 AGAGAAGATGA Db 7916 AGAGAAGATGA	1140	Qy 1200 ATTATGTCAA

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ATGGATGATGAGGAGACTGTGGCCCTGATCGCG 1319
                                      TGTGTGTACCCCATCAGCGTGGTCCCGCAGGCC 59
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                                                                                                                                                                                                                                                                       ma subdivision; Enterobacteriaceae;
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DNOWVOLOLEKTWPENGWGEKTISFAGTEWYLRWGGPDSDVPQPRSLEVEVRTKEET
SALVSLRSSVVRE"
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AGMLPRPELQWVGYRLRQQKLERLSYFHVDHPSGVSPDVRVMLDGVHAFRLRFFVNGD
WQARWDSTGILPQAVEVTLVMDDFAELPRLFLVSKETAE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"Type II secretion pathway related protein"
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Pred. No. 0;
0; Mismatches
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/transl_table=11
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/protein_id="BAA31764.1"
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9193. .9540
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9537. .10136
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llarity 99.9%;
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Best Local Similarity
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                                                                                                                       LSGYRLIPGKHSSLFYNAGLHDNDLAVSVNGSELRDTRQAQQIMKQLPELKEIKITVE
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239

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Db 77611 ATCAGGGAAGCTTTTTCACGTATGGCATGGAT	Qy 1320 GGAGGCATACATTTGGTAAAGCACATGGTGCAG	1380	77731	Db 77791 GGAAACGGGAAATATRACATCACCAGTGGCCTGG	1	AX19172	ACCESSION AX191725.1 GI:15209894 KEYWORDS	SOURCE Escherichia coll. ORGANISM Escherichia coll Bacteria; Proteobacteria; gamma subd	REFERENCE 1 (Dases 1 to 92721) AUTHORS Inverser, but, but, but, but, but, but, but, but	ΑΓ	FEATURES Locality (2007) PEATURES 1. 92721 source //crganism="Escherichia coli	AdD_xret="taxon:552" BASE COUNT 24870 a 20267 c 23868 g 23716 ORIGIN	Query Match 99.2%; Score 1476.4;	Matches 1488; Conservative 0; Mismatche	r	1000	Db 76411 ATGATTTTTGTCACAGCTCAATGCTACGGAC	Qy 120 AGCCAGTTAAGCCAGGGTTTCCCTGCTGAAAAA	180	Db 76531 AGGCGGGGGAACTCCGTCCGGCCAGTGAACCGT	Qy 240 CGGCGCTGATACCGGCAGAAGATGGTCGCAAACTC	76591	Db 76651 GATACCTTCGTCAACACGTACAAACCAAA	360		Qy 420 ACCCTTAGTATTTTTGTCTGTAGTATCTATCCT
	CGTCC	76591 CGCCGTGATACCGGCAAGATGGTCGCAAACTCCCGCTCCGTGCAGCGGCCTATTTCAG 76650	300 GATACCCTTCGTCATCACACGTACAAACCAGAAGACCAGCTTTTTGTTTCTGACATCCA 359	CAAAGAAAGGGAATATTCAGGTCTGCGCAGCACTCAACGGCATCGTCAGTTGCGGCTTGGA 4	caaagaaaggaagattcaggtctgcgcagcactcaacggcatcgtcagttgcggcttgga 76	420 ACCCCTTAGTATTTTTGTCTGTAGTATCTATCCAGCAATAGGTATATCCTGTTGCATC 479	480 AATAAAGTTGACTTTTGTATACAACATGCGAATTTCCCTTAATCCGGAGCTATTCGTATG 539 	540 ATABARARA CTCTTCCTGTTCTGATTCTTCTGGGGGGGGGGGGGGGG	76891 ATAAAAAAAACCCTGTTCTGATTCTTGGGGGCTATGGGGGGGG	76951 GTAGCCGCTGATAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAACT 77010	660 CCTCTGAGATTACACAGCCCTGAATCAATCCTGGGGGGCTGATTTTGATTATGCCACC 719	AGATITCAACAGCIGGATAIGGAGGCICIGAAAAAAGATAICAAAGATITGCIGACAACI	77071 AGAITTCAACAGCTGGATATGGAGGCTCTGAAAAAGGTATCAAAGATTTGCTGACAACT 77130		TGGCACGGTGCCGGAACATACAGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAG	77191 TGGCACGGAGCGGAACATACAGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTAG 77250	900 CAACGTTTGAACCGCTGAACAGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTGG 959 	TIGCTGGGCGGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAACCTGATGGTC 1019	TIGCIGIGGCCAGICAAGAAAAATACGGCICCAGIATITCCIGGGGAGACCIGAIGGIC 773	1020 CTGACTGGTAATGTTGCCCTTGAATCCATGGGATTAAAACGCTGGGATTTGCTGGCGGA 1079	AGAGAAGATGACTGGGAGTCGGACTGGTATACTGGGGGGCCTGACAACAAGCCTCTTGCA		1140 GATAACCGGGATAAAACGGGAAACTTCAGAAACCTCTTGCCGCCAGAGGGGACTT 1199	77491 GATAACCGGGATAAAAACGGGAAACTTCAGAAACCTCTTGCCGCCACGCAGATGGGACTT 77550	1200 ATTTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGAT 1259 [260 ATCAGGGAAGCTTTTTCACGTATGCCCATGGATGATGATGAGGGAGACTGTGGCCCTGATCGCC 1319
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COTGCCACACTCCGGGCAGTACATGCCGC 239
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                GATGAGGACTGTGGCCCTGATCGCG 77670
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                                                                                                                                                                                                     Submitted (22-JUN-1995) W. Brunder, Universitaet Wuerzburg,
Submitted (22-JUN-1995) W. Brunder, Universitaet Wuerzburg,
Institut fuer Hygiene und Mikrobiologie, Josef-Schneider-Strasse
D 97080 Wuerzburg, FRG
2 (bases 1 to 2407)
Brunder,W., Schmidt,H. and Karch,H.
Brunder,W., Schmidt,H. and Karch,H.
March an onvel catalase-peroxidase encoded by the large plasmid of
enterobaemorrhagic Escherichia coli 0157:H7
Microbiology 142 (Pt 11), 3305-3315 (1996)
                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 2407)
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0157:H7 katP gene for EHEC-catalase/peroxidase
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Pred. No. 1e-311;
); Mismatches 1; 1
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131. .2341
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1. .2407
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EHEC-catalase/peroxidase;
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                                                                                                                        TGGCACGGTGCCGGAACATACAGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAG
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ORGANISM	REFERENCE AUTHORS	TITLE	PUBMED REFERENCE AUTHORS	TITLE	JOURNAL FEATURES SOUICE	eueb	CDS			•				dene	CDS			_
OY 587 CITITCTACCGCTGTAGCCGCTGATAAAAAGGAGACTCAAAATTTCTACTACTGCAGAAAC 646	OY 647 ACTGGATTTAACTCCTCTGAGATTACACAGCCCTGAATCAAATCCCTGGGGGCTGATTT 706	QY 707 TGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTCTGAAAAAAGATATCAAAGA 766 	QY 767 TITGCIGACAACTICCCAGGATIGGIGCCCTGCGGAATAIGGICCAITAIGGICCTITCIT 826	QY 827 TATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACATATGATGGCCGGGAGGCGC 886 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 887 CAGTGGTGGTCAGCAACGTTTTGAACGGCTGACAGCTGGCCGGATAACGTTAATCTGGA 946	OY 947 TABAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGG 1006	QY 1007 AGACCTGATGGTCACTGGTAATGTTGCCCTTGAATCCATGGGATTAAAACGCTGGG 1066	OY 1067 ATTTGCTGGCGGAAGAGATGACTGGGAGTCGGACTGGTATACTGGGGGCCTGACA 1126 	QY 1127 CAAGCCTCTTGCAGATAACCGGGATAAAAGGGGAAACTTCAGAAACCTCTTGCCGCCAC 1186	QY 1187 GCAGATGGGACTTATTTATGTCAAATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGC 1246 	OY 1247 TTCCGCGAAAGATATCAGGAAGCTTTTTCACGTATGGCCATGGATGATGAGGAGCTGT 1306 	QY 1307 GGCCCTGATCGCGGGGGCCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAA 1366 	QY 1367 AIGTAITGGCGCAGGGCCTGATGGTGCACCTGTGGAGGAGCAGGACTGGGATGGAAAAA 1426 	OY 1427 TAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTC 1486 	QY 1487 GAC 1489	Db 1081 GAC 1083	AED13690/C LOCUS AE013690 12268 bp DNA linear BCT 26-JUL-2002 LOCUS AE013690 DEFINITION YERSINIA PESTIS KIM Section 90 of 415 of the complete genome. ACCESSION AE013690 AE009952 VERSION AE013690.1 GI:21957603	SOURCE Yersinia pestis KIM.

gene

gene

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LSIKVSSPDVEIGALSGGNQGKVVIGRSLITRPNILLLDEFTRGIDVGAKADVFEMMV
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//Gene-"Y087"
//Gree-"Y087"
//Gree-"Y087"
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carbohydrates, organic acids, alcohols"
carbohydrates 1 to 356 of 381 are 59.83 pct identical to
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(AL603643) probable sugar ABC transporter permease protein
[Sinorhizobium mellloti]"
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ILDNAGSDATIGPIKKAKAAGIPAFLIDREINETGIAVSOLVSNNYQGAQLGAEKFYT
LAGGKGKYIPLIGRESDTHAVPRSQGFPUVIDBENBENDKWVAQQTANWSQTBAPNRMES
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3893. 4510
3893. 4510
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//function-"putative transport: residues 1 to 344 of
/note="sugar (D-ribose?) transport: residues 1 to 344 of
/note="function pot idention to residues 1 to 344 of 344
from GenPept : >pplAaD37310.1|AF135170_1 (AF135170) ribose
ABC transporter [Yersinia pestis]"
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VETEGREGIRLAIDGDEQVLQLGPIVKGNAIRDASFFIRFDDFKNQVQYAQLAKALS
LRALQEVAKRDASWIGQQVEVLAAVTLIPPTSLSNGVPLSLNKESH"
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//function="residues 1 to 205 of 205 are 100.00 pct identical
//focte="residues 1 to 205 of 205 from GenPept :
- residues 1 to 205 of 205 from GenPept :
- ypl|AAD37311.1|AF135170_2 (AF135170) unknown [Yersinia
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4510. .6033
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/gene="y0875"
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/gene="rbsC"
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>gb|AAD36032.1|AE001758_10 (AE001758) hypothetical protein [Thermotoga maritima]*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2252
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                                                                                                                                                                                                                                                                                                  /function="enzyme; central intermediary metabolism: Pool, multipurpose conversions"

multipurpose conversions"

/note="residues 6 to 490 of 495 are 40.36 pct identical to residues 7 to 494 of 502 from E. coli K12 : B3926; residues 6 to 490 of 495 are 44.35 pct identical to residues 4 to 479 of 489 from GenPept : >pp|AALA2899.1|
(AE009144) glycerol kinase 2 [Agrobacterium tumefaciens str. C58 (U. Washington)]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 GACTITGTATACAACAIGCGAATITCCCTIAAICCGGAGCTAITCGTAIGATAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2369 AATCATGTTAAAAATAGTTGCCTTTTAGTTAAAGGGGACTTAT--ATATGTTAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549 ACTCTTCCTGTTCTGATTCTTGGGGGCGGGGGGGGGGTTTTCTACCGCTGTAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2311 ATCTTACCCGTACTAATAACTCTCGCCATTGTACATAATACACCTACGGCTTGGGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             609 GATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAACTCCTCTGAGA
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'note="disrupted by frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="y0877"
/function="unknown"
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                                                                                                                                                                 /note="y0876"
9196. .10683
/gene="glpK"
                                                                                                                            /gene="glpK"
/note="y0876"
9196. .10683
                                                                                   .10683
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SENDNOPERABLE SARKATEGYTLYLASHODDNKONQLETALIARKATILDNA
GSDATIGPLKKAKAAGIPAFLIDERINETGAVSOTVSNNYGGAOLGAEKFYTLMGGK
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3221. 5434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEQADILILLEBETSALSKTEVDVLFRYTRELTGOGS IVISRLEBERATGOTITL
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RIRFGMSLVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGKSTLMKITAGVQQQTSQQIYLNGQKYSIANTREAAALGIGWYHQELNLSENLNVAE
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                                                                                    Garcia, E., Nedialkov, Y.A., Elliott, J., Motin, V.L. and Brubaker, R.R. Direct Submission
Submitted (16-MAR-1999) BBRP, Lawrence Livermore National Lab, 7000
                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"mnhrpdivmraedismrfpgtlaldsvnytvyrgkvnviigeng
comosomally encoded catalase-peroxidase of Yersinia pestis
Bacteriol. 181 (10), 3114-3122 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
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/note="ORF2; hypothetical protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                          transporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="antigen 5; KatP homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="catalase/peroxidase"
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                                                                                                                                                East Ave., Livermore, CA 94550, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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/gene="rbs8"
                                                                                                                                                                                                                                                             complement(<1. .1034)
                                                                                                                                                                                                                                                                                              complement(<1. .1034)
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/gene="katY"
                                                                                                                                                                                                                                                                            /gene="rbsA"
                                                                                                                                                                                                                                                                                                                     /gene="rbsA"
                                                                          (bases 1 to 13632)
                                                                                                                                                                                      1. .13632
   chromosomally
                                                             10322012
                                                                                                                                                                                            source
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                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                 gene
                                                             PUBMED
                                                                              REFERENCE
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                                                                                                                                                                       FEATURES
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Yersinia pestis ribose ABC transporter (rbsA) gene, partial cds;
D-ribose binding protein (rbsB), catalase/peroxidase (katī),
cytochrome c (cybC), cytochrome b (cybB), dimethyl sulfoxide
reductase subunit C (dmcC), dimethyl sulfoxide reductase subunit C (dmcC), dimethyl sulfoxide reductase subunit B
(dmsB), dimethyl sulfoxide reductase subunit A (dmsA), and
L-ribulose-phosphate 4-epimerase (araD) genes, complete cds; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [ [bases 1 to 13632] [Garcia, E. ] [Garcia, E., Notin, V.L. and Brubaker, R.R. Molecular characterization of KatY (antigen 5), a thermoregulated
                                                                                                                                                                                                                                                                                                   1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGCCTGAT 1388
                                                                                                                                                                                                                                                               1892
                                                                                                                                                                                                                                                                                                                         AATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAA 1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCTGGATATGGAGGCTCTGAAAAAAATATCAAAGATTTGCTGACAACTTCCCAGGAT
                              GAACCGCTGAACAGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGG
                                                                                                                                                                                                                                                   CCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGT
                                                                                                                                                       GCCGGAACATACAGGACATATGATGGCCGGGGGGGCGCCCAGTGGTGGTCAGCAACGTTTT
                                                                                TGGTGCCCTGCGGATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1449 AAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGAC 1489
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF135170.1 GI:5002118
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FWTASSVDDLYFGSNPELRAVAEVYASDDAKEKFVHDFTKVWEKVWNLDRFDIKNN*
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GNIQEVKKSVGEVINIRNTYHSRYR"
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IPDYGSLMVWRLVLLVLGLGCWICPLIRGRRPWTLVWVLGTLLIIAGELIGRSVFYGL
KCLGAAPGEAGLEQQGLGWANKCGSGNGKDTITSGLEGAWTTDPTHFTWQYLSNLYKH
EWVLTKSPAGAWQWRPKNAANVVPDATDPTKFHPLAMFTTDIALKVDPEYKKITTRFL
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/protein_id-"AAD37318.1"
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/gene="dmsB"
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/gene="cybC"
/note="similar t
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5511.
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/gene="cybB"
6042. .6572
/gene="cybB"
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complement(12089. .12859)
/gene="arab"
/note="arab"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489 GACTITIGIATACAACATGCGAATTTCCCTTAATCCGGAGCTATTCGTATGATAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429 TATTTTTGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 ACTCTTCCTGTTCTGATTCTTCTGGGGCTATCGGGGGAGCTTTTCTACCGCTGTAGCCGCT
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Pred. No. 1.5e-148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(12089. .12859)
                                                                                               complement(9176. .11647)
/gene="dmsA"
                                                                                                                                  /note="similar to
                                                                                                                                                       /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.0%;
                                                                                     /gene="dmsA"
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Matches 740; Conservative
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(URL, http://www.sanger.ac.uk/Projects/Y_pestis/).
Location/Qualifiers
1. .220050
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/protein_id="ch092452.1"
/db_xref="G1:1598113"
/db_xref-"SPTREMBL:08ZC13"
                                                           /organism="Yersinia pestis"
                                                                                              /db_xref="taxon:632"
/note="biovar: Orientalis"
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/gene="YPO3216"
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/note="PF
                                                                                                                                                                                               complement(191. .715)
/gene="YPO3215"
/EC_number="2.7.1.71"
                                                                                                                                       complement(191, .715)
/gene="YPO3215"
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/trans1_table=11
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/gene="YPO3217"
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/gene="YPO3217"
                                                                                /strain="C092
                                                                                                                                                                            /note="aroL"
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                          FEATURES
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Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G.,
Prakhill, J., Wren, B.W., Thomson, N.B., Churcher, C., Mungall, K.L.,
Bractice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungall, K.L.,
Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M.,
Falllingworth, T., Cronin, A., Davies, R.W., Davies, P., Dougan, G.,
Feltwell, T., Hamilin, N., Holtroyd, S., Jagels, K., Leather, S.,
Karlyshev, A.V., Moule, S., Oyston, P.C.F., Quail, M., Rutherford, K.,
Genome sequence of Yershia pestis, Whitehead, S. and Barrell, B.G.
Genome sequence of Yershia pestis, the causative agent of plague
Nature 413 (6655), 523-527 (2001)
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                                                                                    1028
                                                                                                      AATGTIGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGAT 1088
                                                                                                                                                                                                                                                                                                                      Notes: Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web.
                                               3652
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                 CCAGICAAGAAAAATACGGCTCCAGIATTTCCTGGGGAGACCTGAIGGTCCTGACTGGT
                                                                                                                                                                                     GACTGGGAGTCGGACCTGGTATACTGGGGGCCTGACAACAACCTCTTGCAGATAACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04.0CT-2001) Submitted on behalf of the Yersinia
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ414156 220050 bp DNA linear BCT 06-Yershia pestis strain CO92 complete genome; segment 16/20. AJ414156 AL590842 AJ414156.1 GI:15981150
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/note="Similar to Rhizobium meliloti phospholipid
N-methyltransferase PmtA TR:AAG10237 (EMBL:AF201699) (200
N-methyltransferase PmtA TR:AAG10237 (EMBL:AF201699) (200
Bradyrhizobium japonicum PmtA protein TR:Q9LCT2
(EMBL:Y09633) (199 aa) fasta scores: E(): 0.0057, 24.2% id
in 17% aa, and to Klebsiella pneumoniae hypothetical 22.7
kcores: E(): 0, 52.9% id in 191 aa"
/codon_start=1
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/protein_id="CAC92451.1"
/db_xref="G1:15981152"
/db_xref="sprawbi:082C14"
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SARQIADOEYDVPCCLIPLISIPTKISIRILQOTQQRLRARNGYLVLFQYSHLSESLLS
RYFNWKKIRVVRNFPPALVYICHPN"
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ikniasphylsivacsikkaaakmrls"
                                                                                                                                                                                                                                         /product="shikmate kinase II"
/product="shikmate kinase II"
/protein_id="CAC92450.1"
/db_xxef="GI:15981151"
/db_xref="sprexbi:082C15"
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/ARVENGEGWOFRLRESMALQAYTAFKTVVATGGGAVLSSENRAFMRDHGRVIYLRA
SAAVLAKRLAEDPERGRPSLTGKPIVEFILDYLASREALYQDVAHHYLDGTQTPSLV
VEQILQMLTGEMVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Fight" match to entry PF01202 SKI, Shikimate Kinase, foote="Fight" match to entry PF01202 SKI, Shikimate Kinase, score 245.00. E-value 1.1e-69"
complement(470. .544)
/gene="FF03128"
complement(668. .691)
/gene="FF0315"
/note="FF0315"
/note="FF0315"
/gene="FF0315"
/gene="FF0316"
/gene="FF0316"
                               Arol SW:AROL_ECOLI (P08329) (174 aa) fasta scores: E(): 1.5e-31, 55.4% Id in 168 aa, and to Erwinia chrysanthemi shikimate kinase Arol or Arow SW:AROL_ERWCH (P10880) (173 aa) fasta scores: E(): 0, 63.7% Id in 168 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shikimate kinase,
/note="Similar to Escherichia coli shikimate kinase
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                                                                                                                                                         /product="conserved hypothetical protein"
/protein_id="CaC92453.1"
/db_xref="G1:15981154"
/db_xref="SPTRMBL:082C12"
/translation="MQAAADKKLTNIEIQQGLAESLPFADQSFDIVISRYSAHHWHDV
STEALREVREVLERGGKVIFMDVVSPGHPVLDTYLQTVEVLRPTSPHRYSPGFMLSLF
TEGGIVIEWTSDFRYLEFSSWVARMRTPAHFATAIREFQKLASDGVINHYAIQADGS
FTSDIMMIVAVRD
                       YafE SW:YAFE_ECOLI (P30866) (207 aa) fasta scores: E(): 0, 65.1% id in 169 aa, and to Pseudomonas aeruginosa YafE or PA3119 TR:087011 (EMBL:U93274) (187 aa) fasta scores: E(): 0, 55.2% id in 172 aa*
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/translation="MGPVSETSKEGFVKKKKLAICAILRDLGKNDFAVMVTHARGGFI
/translation="MGPVSETSKEGFVKKKKLAICAILRDLGKNDFAVMVTHARGGFI
STILDIOPETNGFIFDFGSVENENVLALGABOLITIVEPTGARIEFTCNKLKKHFFLS
LPARSSAIPPOLYFTORREYFRVSIPOMPAYCSGKFPDGTQXYTLADISLGGMGIY
AMKGSEFPLGGCSVLRDAAVDLGGFGLFKLDLQFIRALDKQVVNNKGEMLTVQRLSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative membrane protein"
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/db_xref="GI:15981155"
/db_xref="SPTREMEL:085C11"
/translation="MEGSYMGISEESIRRITNEKNAVGHSAKWVAIISAVYFIIMLF
YKHBLGVLTLAGGIFLVSFTTWMKKRQKVKSYKNQLQQIEEDKTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Similar to Escherichia coli hypothetical protein
rcgR SW:YCGR_ECOLI (P76010) (244 aa) fasta scores: E(): 0,
40.7% id in 241 aa"
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for YPO3219 by TMHMM2.0"
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/product="gamma-glutamyl phosphate reductase"
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/db_xref="GI:15981156"
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/transl_table=11
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complement(4554. .5813)
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/gene="YPO3219"
complement(3016. .3285)
/gene="YPO3219"
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/gene="YPO3220"
complement(2249. .2770)
/gene="YPO3218"
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                                                              /translation-"MNLLEHWCKAAKOASWOLAMLSTAKKNOALAVIANLLESESQTI
LQANERDWAAARESGMSEALLDRLLLTPARLAAIANDVRQVCRLNDPVGRVIDGSLLD
SGLKLERRRVPLGVIGVIYEARPNVTIDVASLCLKTGNAVILRGGKETHYTNQATVNV
                                                                                                                            IQRALEQCGLPAAAVQAIESPDRQLVNELLRLDRYVDMLIPRGGASLHKICREGSTIP
VITGGIGVCHTFVDENADFERALLVYENAKTQRPSACNSLETLLVHQAVAKTFLPLLS
ARMHAFGYTLHASPLAMPYTADGRAKVVAVEAADYDDEWLSLDLNVDIYYDIDAAIDH
IREHGTSHSDAILYSELSHAEYFVRAVDSSAVYVNASTRFTDGGQFGLGAEVAVSTQK
LHARGPMGLDALTTYKWIGYGDDLVRS"
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                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF00171 aldedh, Aldehyde dehydrogenase family, score -217.90, E-value 0.00013" (complement(4776 . 4841) /gene="YP03221"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTTTTTGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 ACTCTTCCTGTTCTGATTCTTCTGGCGCTATCGGGGAGCTTTTCTACCGCTGTAGCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0; Mismatches 319;
/protein_id="CAC92456.1"
/db_xref="G1:15981157"
/db_xref="SPTREMBL:Q8ZC09"
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complement(5823. 6926)
/gene="YPO3222"
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complement(5823.
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1427 TAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTC 1486
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GAASGKYLGPAPEAAGIEEQGFGWKNSYGSGKGKDTITSGLEGAWTVTPTHWSHNYLD
NLFNENWYKTKSPGGAIOWYPENSNASSAWYDDAFDSFKRHAPYMLTTDLALKEPDYYS
KTARRPLDNAFEDDAFARWFKLIHRDWGPRSRYLGSLYPKEAMIWODPYPPYDYKL
VDANDIANLKGKILNSGLTTSELVKTAWASASTFRGTDRGGANGBAIRLAPOKDWRL
NDPQELAKVLKTLESIQNNFNNAQADGKKISLADLIVLGGMARAIRCARGYDIIVP
FTGRRUDATGORTOWSFSFRYLDFRADGFRNYFDANIWSPPEMLVEKASLIKLSVPEM
FTYLVGGMRVLANNFGOROVGYPTDRGGTLNNDFFINLLSMSTEWKSSETBGTYBGTE
RKTGKLKKWRATSVDLIFGANSELRAVBEATADDAKEKFLODFINAWVKWTADRFDI
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LSplropnatsnpwgerfnyaeeffnsldlaaviedlkklattsodwwradkongfle
Trbshahaacytriydergabargforpaponswidharrllwpirgkyrkis
Wadllylagnyamesgrfiigfagreddwraftliniwgpegkwiesrrodkoklek
PlaatywgliyvnpegpngvpdplaaaekIretfgrwamndeetvaliagghafghth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
Legionellaceae; Legionella
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                                                                                   GGTGCACCTGTGGGAGGAGGAGGACTGGGAAAAAAAATGTGGTACAGGAAACGGC
          GACTGGGAGTCGGACTGGTATACTGGGGCCTGACAACAAGCCTCTTGCAGATAACCGG
                         AATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAA
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/organism="Legionella pneumophila"
/strain="AMSil"
/db_xref="taxon:446"
203. 245?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEMS Microbiol. Lett. 176 (2), 339-344 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legionella pneumophila (strain:AM511) DNA
Legionella pneumophila
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/protein_id="BAA78342.1"
/db_xref="GI:4996128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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AB017595.1 GI:4996127
ARIA; Catalase-peroxidase.
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/gene="katA"
/codon_start=1
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Legionella pneumophila
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203. .2452
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LSPLRQPNATSNPMGEKFNYAEFENSLDLNAVIEDLKKILMTTSQDWWPADYGNYGPLF
INWSWHAAGTYRTYDGRGGANGGFORFAPADNSWPDNALLDKARRILMPYTGNYGRYGIS
INWSWHAAGTYNGYAEGNGGFRUIGFAGGREDARBAIN INWGPEGRWLESKRODKDGKLER

PADLI VLAGNVARESMGFKTIGFAGGREDARBAIN INWGPEGRWLESKRODKDGKLER

GAASGKYLGAPABAAGIENGOFFGWARSYGSKGKKOTTTTGGLEGAWTYPFTWSHYYLO

MLENFWNYKTKSPGGAIONYPENSASSWYPDAFDSESKHAPWLITTDLAIKFDPYS

KIAKRFLDNPKEFDDAFARAWFKLIHRDMGPRSRYLGSLVPKEAMIWQDPYPPYDYKL

VDANDIABLKGKIINSGLYTSELVKTAWASSSTFGTDMRGAMGAPPTRYD
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complete
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NDPQELAKVLKTLESIQNNFNNAQADGKKISLADLIVLGGNAAIEQAAKQAGYDIIVP
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RRIGKLKWRATSVDLIFGANSELRAVAEAXATDDAKEKFIQDFINAWVKVMTADRFDI
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                                                                                                                                                                                                  gamma subdivision; Legionellaceae group;
                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 5249)
Bandyopadhyay, P. and Steinman, H.M.
Direct Submission
Submitted (09-JUN-2000) Biochemistry, Albert Einstein College of
Medicine, 1300 Morris Park Avenue, Bronx, NY 10461-1602, USA
Location/Qualifiers
1. .5249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sednence
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GenBank Accession Number AB017595"
/replace="g"
                                                                                                                                                                                                        Legionellaceae; Legionella.

1 (bases 1 to 5249)

Bandyopadhyay, P. and Steinman, H.M.
Catalase-peroxidases of Legionella pneumophila: cloning gene and studies of KatA function
J. Bacteriol. 182 (23), 6679-6686 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="compared to Legionella pneumophila katA
GenBank Accession Number AB017595"
                                                                                   5249 bp DNA linear BCT pneumophila catalase-peroxidase (katA) gene,
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2386. .4635
/gene="katA"
2386. .4635
/gene="katA"
/note="KatA; localized in periplasm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.8%; Score 384.8; DB 1; 65.8%; Pred. No. 3.1e-103;
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/protein_id="AAG37106.1"
/db_xref="GI:11528085"
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Legionella pneumophila
Bacteria; Proteobacteria;
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Legionella p
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AF276752.1
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KEYWORDS
SOURCE
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AUTHORS
                                                         RESULT 11
AF276752
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TITLE
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Escherichia.
1 (bases 1 to 1829)
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                                                                                                                                                                                                                                                                                                                     AGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGA
                                                                                                                                                                                                                                                                                                                                                                         1010 CCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATT
                                                                                                                                                                                                                                                                                                                                                                                      1187 GCAGATGGGACTTATTTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGC
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                                        GGATTTAACTCCTCTGAGATTACACAGCCCTGAATCAAATCCTGGGGGGGCTGATTTTGA
                                                                                            710 TTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTCTGAAAAAAGATATCAAAGATTT
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X17114 S79575
X17114.5 GI:21038833
insertion sequence; trpA gene; transposase. Escherichia coli.
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                                                                /translation="MLPRFADIFOGGNRWLNWLEKQPEGSVRPVVTESVTKIMACGTT
LMGYTGWCCSSPDCCHTKKVCFRCKSRSCPHCGVKAGAQWIQYLLSLVPDCPWQHIVE
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HLSTTAGGYYSGHTWRKNLHFYARKYMSWMRYRITRLLSRKYPELVIFDELAVEGNSKR
DWNCFLDTHYRRGWYNYRISYMDNATHVAVYFGSYLKKPPVPWSRLEHYAGOBEIGLR
YNSHRYKREEYLLMSGDEFMERFSWHVADSKGFRWVRYYGFLSPVKRRLLEEVVYVITE
TVRKTAMQIRWRGMYQRLLKVDPLKCILCGSQMRFTGIKRGYRLAEHVANDFRAROO
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Pred. No. 2.6e-98;
0; Mismatches 15; Indels
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Robertson,D.E., Sanyal,I. and Adhikary,R.S.
Catalases
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Pred. No. 3.5e-95;
0; Mismatches 264;
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Location/Qualifiers
1. .2238
/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2238 bp
Sequence 7 from patent US 6074860.
AR098264
AR098264.1 GI:12807521
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/db_xref="G1:21038834"
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66.7%;
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Best Local Similarity 66.7
Matches 542; Conservative
                                                                                                                                                                                           429 c
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.0
Matches 388; Conservative
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ORIGIN
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VERSION
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ORIGIN
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fddayeccadlnipffydagnkklyfwfyryddegypeiarcterefatilagisagg
                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (23-APR-2002) Garcillan-Barcia M.P, Biologia Molecular,
niversidad de Cantabria, C/ Herrera Oria s/n, Santander, Cantabria,
                                                                           2 (bases 1 to 1829)
Mendiola,M.V. and de la Cruz,F.
Mendiola,M.V. and de la Cruz,F.
S191 transposase is related to the rolling-circle-type replication proteins of the pUBLIO family of plasmids
Nucleic Acids Res. 20 (13), 3521 (1992)
                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27-cort-2000) F. de la Cruz, Departmento Biologia
Submitted (27-cort-2000) F. de la Cruz, Departmento Biologia
Molecular. Un., Crartabria, Facultad Medicina, C/Cardenal Herrera
Oria s/n, 39011 Santander, SPAIN
revised by [5]
Cpases I to 1829)
Garcillan-Barcia,M.P.
                                                                                                                                                                                                                       Submitted (06-Nov-1989) F. de la Cruz, Departmento Biologia
Molecular. Un., Cantabria, Facultad Medicina, C/Cardenal Herrera
Oria s/n, 39011 Santander, SPAIN
 Mendiola,M.V., Jubete,Y. and de la Cruz,F.
DNA sequence of IS91 and identification of the transposase gene
J. Bacteriol. 174 (4), 1345-1351 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7. 2002 this sequence version replaced g1:20376803. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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38. .43
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/note="ORF 121"
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303. 308
/gene="tmpA"
326. 331
/gene="tmpA"
372. 378
372. 378
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454. .1641
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/note="r
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Direct Submission
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Linton, L., McEwan, P., McKernan, K., Talamas, J., Tirrell, A., Ye, W., Zimmer, A., Barber, R.D., Cann, I., Graham, D.E., Grahame, D.A., Guss, A., Hedderich, R., Ingram-Smith, C., Kuettner, C.H., Krzycki, J.A., Leigh, J.A., Li, W., Liu, J., Mukhopadhyay, B., Krzycki, J.A., Leigh, J.A., Li, W., Liu, J., Mukhopadhyay, B., Reeve, J.N., Smith, K., Springer, T.A., Umayam, L.A., White, O., White, R.H., de Macarlo, E.C., Ferry, J.G., Jarrell, R.F., Jing, H., Macarlo, A.J.L., Paulsen, I., Pritchett, M., Sowers, K.R., Swanson, R.V., Zinder, S.H., Lander, E., Metcalf, W.W. and Birren, B. Physiological Diversity and Physiological Diversity Common of M., 532-542 (2002)
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Submitted (20-MAR-2002) Center for Genome Research, Whitehead
Institute, Nine Cambridge Center, Cambridge, MA 02141, USA
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Methanosarcina acetivorans str. C2A, section 107 of 534 of the
Complete genome.
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Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
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1 (bases 1 to 11310)
Galaqan.J.E., Nusbaum.C., Roy.A., Endrizzi,M.G., Macdonald,P.,
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FLSYRLGNOISLDBATILSVANGHYNELGHYNELHEGELKEGERIKH
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1 2495 c 2699 g 3049 t
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ORIGIN
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1 (bases 1 to 17986)
Xu,D.Q., Cisar,J.O., Ambulos,N. Jr., Burr,D.H. and Kopecko,D.J.
Molecular Cloning and Characterization of Genes for Shigella sonnel
                                                                                                                                                                                                                                                                Shigella sonnei
Shigella sonnei
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                             AF294823 Shigella sonnei O antigen gene cluster, complete sequence: insertion sequences ISI InsB (insB), InsA (insA), IS630 transposase, IS629 ORFA (orfA), IS91 transposase (insB) and AF294823
AF294823.1 GI:15149169
                                                                                                                                                                                                                                                                                                                              Shigella.
                                                                         RESULT 15
AF294823
LOCUS
DEFINITION
                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
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GGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGA 1488

CATACATITIGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGCCT

1326

1386 9762 1446

GAAGCTTTTTCACGTATGCCCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGAGGG

23.5%; Score 349.4; DB 1; Length 11320; llarity 66.6%; Pred. No. 1.5e-92; Conservative 0; Mismatches 266; Indels 9;

Query Match Best Local Similarity Matches 548; Conserv

FEATURES

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SIDLFILKEYESYNSYAIYONYTRNATGLITYFNYTYTVLLSFSYYLKNSFGNIRR
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I SLTLLVY I SSAYFVCI SSGRFSLLQAVGRFRCELY I NIY STI I Y I GCNLFLSLFI EP
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AKVIENTQRDVNIALINELSIIFNKLGIDTLEVLEAAGTKWNFLPFRPGLVGGHCIGV
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1666. .1671
70cte-"putative promoter of O-antigen biosynthetic operon"
1745. .3069
1745. .3087"
1745. .1749
1756. .3069
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                                                                                             Yu,D.Q., Cisar,J.O., Ambulos,N. Jr., Burr,D. and Kopecko,D.J.
Direct Submission
Submitted (109-AUG-2000) Oral Infection and Immunity Branch,
National Institutes of Health, National Institute of Dental and
Craniofacial Research, Bldg. 30, Room 302, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MYAFTAKEQWTAKTYIQAPRIAELGSYLKFHQAYARILNQPLDT"
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Form I O Polysaccharide: Proposed Biosynthetic Pathway and Stable Expression in a Live Salmonella Vaccine Vector Infect. Immun. 70 (8), 4414-4423 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to Escherichia coli IS1 InsB"
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complement(734..739)
complement(756..761)
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9 (sites)
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                                                BCT 10-JAN-2001
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Extremophiles 9. strain C-125
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Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G.,
Sasaki, R., Hirama, C., Fuji, F. and Masui, N.
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halodurans C-125
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Extremophiles 3 (3), 227-233 (1999)
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Bacillus halodurans genomic DNA,
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AP001510.1 GI:10173440
                                                                                                                                              Bacillus halodurans DNA
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Takami, H.
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                                                                                                                                                                                                                     FGYORSRWSTELLAIKINEITGCOLNAGTVRRWIPSAGIVWRRAAPTLRIRDPHKDEK
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ENPKFRVIYOPVYSPWMNHVERLWOALHDIITRNHOCSSMWOLLKKVRHEMETYSPEP
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SELISHCOMGNDELIGFFGAEIDSLINYTRLSIESCNTEKLFFDARKYSDGHPTYH
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NYPIYDVNNYKAVTLDFSWLAKYDSDYGYYNKKSFSTDISIINLNTGGIELFLSLDEM
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                                                                                                                                                                                                                                                                                                                                                                                                                         (E-mail:takamih@jamstec.go.jp,
URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-66-6364)
Location/Qualifiers
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                                                                                                                                                             Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28 (21), 4317-4331 (2000)
                                                                                         Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Sasaki, R., Masui, N., Fuji, F., Hirama, C., Nakamura, Y., Ogasawara, N., Kuhara, S. and Horikoshi, K.
                                                                                                                                                                                                                                                                                11 (bases 1 to 302150)
Takami, H. and Takaki,Y.
Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Technology Center, Deep-sea Microorganisms Research Group; 2-15
Natsuchima, Yokosuka, Kanagawa 237-0061, Japan
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23. .778
4 (4), 209-214 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="BH0827"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="BH0826"
23...778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="BH0826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="BH0828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/gene="fruB"
775. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="fruA"
1701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             775. .1695
/gene="fruB"
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/gene="fruA"
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Extremophiles
20426005
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                   MEDLINE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83724
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LRGKENVHIELRLVALTAQHKETSDGGSSLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPRGIETTHGTHVAGTVAANGLIKGVAPDANLLAYRVIGPGGRGSTAGVIAGIERAVO
BODIUMULSIGNTLANDDDRATSIALDWAMAEGVVAYTSNGNGSPNNWTVGSPGTSRDA
ISVGATRLPYNKYRASVFTSDGIDYPSADIMGFPSDEELLELDGETYEAFAGLGKPG
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LSNEDGLKMRNELENGQNTVTFSIEFDKLVGETVADDFSSRGPVMHTWMIRPDVSAPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83843 ACAAATAACGACTGGTGGCCAAACGCGTTAAACTTAAATATTCTTCGTCAGCATGACAAA 83784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGSMCTANNY ILGY ILGGMAAYDMGGPINKAAFTFGTAMIDACNFGPHAAVMAGGMYP
PLGIALATTLFKKKFTKQEREAGKTNY ILGASFITEGAIPFAAADPGRYIPSIIYGSA
FAGGLTALFNYTLSAPHGGAFYIFIGNIYNNPLLYLYAIIAGSIYTALLLGFWKKDAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSSSALETVIVEIEDPSIIEAKHQGGKOSKNELKQARGSVIEQIQDLVPSSTVTHEYD
FLFSGFALELPAHQIPSILGIDGVHAVYPNIEYEVETDFDEVVIEKDAYSPEMLDSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIVSTIPTHOPDDPYGYGSROGTSMASPHVAGAAALLLEAHPWGYDHYKAALMYTAE
NLYDENGNRYPHNTOGAGSIRIYDAIESETLYTPGSHSFGTFTKERGKOVEROHFTIH
NLSNKRRTYQFDYQFAGNPDGIKVKTSKNLRYQPGKTOKINFNYQYDARKLDPGYYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIGANDAWEAGYTGEGITVAILDTGVDYTHPDLVHAFGDYKGWDFIDNNDDPQETPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
EMLATIGGGNAFGLMIPVLAAFIAMSIADRPGFAAGMIGGLIASTGEAGFLGGLIAGF
LAGYVALGVRKVLANLPQTLDGIKTILFYPVFNIFITGMIMLVIVGPLAAFNTGLQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 ACTCAAAATTTCTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATTACACAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 681 GAATCAAATCCCTGGGGGCCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          741 GAGGCTCTGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 302150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="minor extracellular serine protease"
/protein_id="BAB04550.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 334.6; DB 1
Pred. No. 8.9e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown conserved protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LISIIVLALFGKKYSQMFQPKKELGV"
COMPlement(5283. .7682)
                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB04548.1"
/db_xref="GI:10173444"
                                                                                                                                                               complement(3677. .4078)
                                                                                                                                                                                                            complement(3677. .4078)
/gene="BH0829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5283. .7682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="vpr"
/EC_number="3.4.21.-"
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4694. .5254
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                                                                                                                                                                                      /gene="BH0829"
                                                                                                                                                                                                                                                                           /note="BH0829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="BH0830
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63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="vpr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                  ELGSELFERSAREVKLTPFGQTFALRVRDILRAVDELGEFARASRDSFLTRLRIGIIP
TLAPVLLPUHKRLMKSFAGIQIEVRETHTGKLVHELAQGOLDMAIVALPVSEPSLTE
LSLFGRIRAGPAPPGRRKVPVERBALREMRLLLLEEGHCFRDQALSFCKVGAARPRE
IMEGSSLSTLVQWYGAGIGITLIPEMAVPVERRAHVSISRFPSPAPRRTIGMYWLNF
HPMGNHLPWKLAKARSRLVWRKTSPSAINGG"
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BGIQKDFNAAQTGARKISLADLIVLAGAAGYKKAAAAGGNAYSVPLFFGRMDASEAQT
BGIQKDFNABPRIDGFRNYNOKRLQFKKPEBMLVDRAQLLTLTGPEMTVLVGGLRVLK
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1051 c 1011 g 570 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCGCTCGGTAAGGACTTCGATTATGCCGAAGATATCCAAGAAGCTCGATCTCGACGCG 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           867 TATGATGGCCGGGGAGGCGCCAGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   688 ATCCCTGGGGGCTGATTTTGATTATGCC-ACCAGATTTCAACAGCTGGATATGGAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.4%; Score 333.6; DB 1;
llarity 66.8%; Pred. No. 5.8e-88;
Conservative 0; Mismatches 259;
                                             /organism="Rhizoblum etli"
/db_xref="taxon:29449"
/plasmid="pCFN42f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(942. .947)
Location/Qualifiers
                                                                                                                            complement(6. .947)
                                                                                                                                                                          complement(6. .932)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="KatG"
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1064. .3260
/gene="katG"
1064. .1070
/gene="katG"
1077. .3260
                                                                                                                                                   /gene="oxyR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1077. .3260
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                                                                                                                                                                                                   /gene="oxyR
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Best Local S
Matches 537
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                              source
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AR486647.1 GI:19702287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83184
                                                                                                                                                                                                                                                                                                                                                                                                                                             83364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83123 TTTGGTAAGGCTCACGGTGCAGGAAATCCAGATCA---TGTTGGTCCAGAGCCAGAAGCT 83067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGAAGATGACTGGGAGTCG 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1272 TITICACGTAIGGCCAIGGAIGAIGAGGAGACTGIGGCCCTGAICGCGGGAGGGCAIACA 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1212 CCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCT 1271
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Rhizobium etli
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                             AGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCCAGTCAAGAAA
                                                                                                                                                                                                                                                                                                 AAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTT
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                                                                                                     AGGACATATGATGGCCGGGGGGGCCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAAC
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/translation="Maplrgwaprgerlugyaprghwwwffyaalradrysapfild
GPINGERFRIYVQQVLVPELKAGDIVILDNLGSHKGQBIRAAIRKAGARLFFLDKYSP
DLNPIEKLFAKIKHWLREAQARSRDAIHDELRHILQAVTPQECAAYFKEAGYERA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MARPFSNDLRERVVDAVTGEGLSCRAAARRFGIGISTAIDWVRR
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WTFVHEEGLSYKKRRWSPANGSGPTSPATGHDG"
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/db.xref="G1:14524460"
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/translation="MDQKSDSAGKCPVAHTAPRGRSNRDWPDQLDVQVLHRHSGLSD
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LESMGFKTFGFAGGRVDVWEPEELFWGPEGTWLGDERYSGERQLSEPLAAVQMGLITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="Elements of external origin; Transposon-related functions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"putative transmembrane transport protein"

*protein_id="AAK65943"."

/db_xref="GI:14524459"

/translation="MTVNVSPTVMFILLISFGTVLGIAGTDLVLPAIPAMPTALGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAQMVLAAYAGGTLVGILITFGELGARYSRRKLLVWSLGLFAVTSLLSAYAPTLEMLVI
LRFAQGAFGSGPAVFAPGFIHGLYPGDKAPSMFGRLGSIESLTPALAPTAGAYLMTVG
GWQTSFLMLAGLAILCAVGSWAYRQSLPDRLEALEVHQSYMSIIRNGDFLRHGLSQAL
SLGSILIFVFGAPAVMTGALGMTIGDFILLQVFGIALFILASNASNALARRFGIERMI
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SRGAALVVAAILGITAGGTAAAAPFINVGWWPLALASSLAALLALLCLKLIGSTA"
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//gene="SMa2377"
/function="Cell processes; Transport of small molecules
/note="glimmer prediction; similar to putative
chloramphenicol transporter in several organisms,
including Salmonella typhimurium, AF118107, Klebsiella
pneumoniae, AAF27726, and Enterobacter aerogenes,
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/function="Cell Processes; Protection responses;
detoxification"
                                                                                               /standard_name="ISRm2011-2/ISRm11"
/note="SMa3018; predicted by homology"
                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="TRm2011-2a transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                                                                                                      /evidence=not_experimental
/rpt_family="ISRm2011-2/ISRm11"
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/db_xref="G1:14524458"
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/db_xref="GI:14524457"
                 /db_xref="taxon:382"
                                        /plasmid="pSymA"
420. .1478
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•989. .1462
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1664. .2833
                                                                                                                                                                                                                            /gene="SMa2373"
516. .923
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AE007314 AE006469
1689 CTGGCGAACCCGCTTGGCGCCGTGCAGGTCTCATCTACGTCAATCCCGAAGGCCCG 1748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.

1 (bases 1 to 10578)
Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P., Barloy-Hubler, F., Bowser, L., Capela, D., Galibert, F., Gouzy, J., Gurjal, M., Bong, A., Huizar, L., Hyman, R.W., Kahn, D., Kahn, M.L., Kalman, S., Keating, D.H., Pelm, C., Peck, M.C., Surzycki, R., Wells, D.H., Yeh, K.-C., Davis, R.W., Federspiel, N.A. and Long, S.R., Mucleotide sequence and predicted functions of the entire
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Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P.,
Barloy-Hubler, F., Bowser, L., Capela, D., Galibert, F., Gouzy, J.,
Gurjal, M., Hong, A., Huizar, L., Hyman, R.W., Kahn, D., Kahn, M.L.,
Kalman, S., Keating, D.H., Palm, C., Peck, M.C., Surzycki, R.,
Wells, D.H., Yeh, K.-C., Davis, R.W., Federspiel, N.A. and Long, S.R.
Direct Submission
                                                                                                                ATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACCTG
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Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9883-9888 (2001)
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/organism-"Sinorhizobium meliloti"
/strain-"1021"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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GIQRDFNAAQTDGKKISLADLIVLAGGAAVEKAAKAGGHDITVPFTPGRADASEAQTD
AASFAALEPRADGFRNYVSTTRQQFNKPEEALVDRAQLLTLTAPEMTVLVGGLRVLKA
GEPKHGVFTSRPEALTNDFFVNLLDMGTQWSPIEGEEGVYEGRDRRTGAARWTGTRVD
LIFGAHGLRAFAEVYAQSDAREKFVKDFVAAWTKVNNADRFDLV"
5640. 6113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MLLKAMKIGRQSLYDTFGDKWKLYCLAVERYSASETSAHIALLR
GKPRALEGIRLVWERVVDNANQACLGVNSICEFGQSRPDLAALHHAADRRLKNVVVER
IREAQAAGDLAVSLPAEAVADFLVANIAGIRIAARGGARREHLQSLSRLALRAVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="glimmer prediction; similar to TED2, a putative quinone oxidoreductase, from Zinnia elegans, BAA06460, and from cowpea, T11672; also similar to putative oxidoreductases from Mycobacterium tuberculosis,
                         EGGA I EDQGLGWKSTFGTGVGKDA I TGGPEVTWSQT PTRWSNHFFENLFNHEWELITKS
PAGAYQWKAKNAEAT I PDAYDPSRKHVPTRLTTDLSLRFDPAYEK I SRRFLENPDEFA
                                                                                                DAFARAWFKLTHRDMGPKVRYLGPEVPAEDLIWQDVIPAVDHRLVDETDIAGLKAKII
ASGLSVQELVSTAWASASTFRGSDKRGGANGARIRLAPQKDWEVNRPAQLARVLSVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKAVVMKEVGGTDVMEFVDRPEPVARPAHVVVEVAAAGVNFMDI
GVRQGMAWTDIPNPKVLGVEGAGRVLAVGDGTGEFAVGDRVAWVYAPGSYAQRQSIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASLVKIPDTVDDRTAASTMMGGLTASHFATDFYPVQPGDIALVHAAAGGVGLLITQII
RIGGGVIGPRSSBDKVATARKAGABITVIDVDGSRADDEVIRITGGEGYNVYYDGSGP
KTFKGSIEBLRRSGFFCWYGPGPLEINNLPKSIKIGYAFFMHHTRELLLDR
TKQLFDWIEDGSIIVTIGETYRLADAAGAHAAMASRATIGKLLLIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLNIIAGTLRPSSGTVAIOGRVALARQILRAGADETIADVFGATOAVAVLRRAEKGDA
SVEELETADWTVEERIYSALARLGILBARADTLLNOLSGGGYTRAVLAAAIFSEPDFLL
LDEPTNNLDRDGRRAVIGLLSGWRSGAIVVSHDRELLEEMDAIIELTSLGTKRYGGGW
SAYQAARAYELBAAQOSLTLARKTADFVDRKARALAERILDKRDASGTRRAAKGDPRIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVGRRKSNAEESRGKSVELAERRRAGALDAVTAAKARIEVLOPFSIRLPRTELPAGRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSVNVPFTLLDQSVSILERGETILENFKRLNPGASDNACRAALASFRFRADAALQRVE
ALSGGQVLRAGLACALGGSDPPSLLILDEPTNHLDIDSIEAVEAGLLSYDGALVVVSH
NPEGPNGNPDPVAAARDIRETFARMAMNDEETVALIAGGHTFGKTHGAGDPSFIGADP
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/note="glimmer prediction; similar to probable ABC
transporter from Streptomyces coelicolor, T35245, and to
VarM (probable transporter for virginiamycin) from
Streptomyces virginiae, BAA96297. ABC transporter family"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MPSITLSALSWSKPDGEHVFSDLDLAFGPERTGLVGRNGIGKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLAFDGVTAGYDPARPIIRDLSFSLVGPRRVSVTGPNGSGKTSLLKVVTGELPPFKGT
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/product="probable ABC transporter, ATP-binding protein"
/protein_id==NaRK65947.1"
/db_xref="G1-14524463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumifaciens, etc. Zinc-bindng family" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="Small molecule metabolism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="probable oxidoreductase"
/protein_id="AAK65946.1"
/db_xref="G1:14524462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"hypothetical protein"
/protein_id="AAK65945.1"
/db_xref-"GI:14524461"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="glimmer prediction"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                        5640. .6113
/gene="SMa2381"
/function="Miscellaneous;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(7357. .8946)
/gene="SMa2385"
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/gene="SMa2385"
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                                                                                                                                                                                                                                                                                                                                 /gene="SMa2381"
5640. .6113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SMa2383"
6167. .7135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SMa2383"
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CDS

/function="Miscellaneous; Unknown"

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4322
                                                                                                                                                                                                                                                                             /function="Cell processes; Adaptation"
//function="glimmer prediction; very similar to Ohr, a putative stress-induced protein, from Bradyrhizobium japonicum, AAF78793"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1160
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                                                                                                                                        TAAELGISKHTLYRRYPNRQALLEAVVERDLVRFRKTLAEAAGGGEAPLAALRDMAFR
YFRFGTDRDYSAFYLSVTAEAVFSLPLRERLAAWSSAALEPLVQAIISAQAAGLVVPG
STIEICHVLIDLLEGANNRVRLCLSESPDASERLRLFESRRAVFGTAMMPEPNRPLGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTG 1400
                                                                                                                         /translation-"MIRARRRAGGRPTREEAEALTRRLLDSARSTFARKGIANSSMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1044 TCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTCGGAC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4321 ACGCATGGCGCCGGCGATCC---GTCGTTCATCGGTGCAGACCCGGAAGGCGGCGCCATA 4265
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prediction; putative bacterial regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1161 AAACTTCAGAAACCTCTTGCCGCCACGCAGATGGGGACTTATTATGTCAATCCTGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4441 CCGAACGGCAACCCCGACCCGGTTGCTGCCGCGCGCGGTATCCGCGAAACCTTTGCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1981 TCCGATCCGCTGGGCAATACGTTCAACTACGCCGAGGAGTTCAAGAAGCTCGACCTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 804 TATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       864 ACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              924 TGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4621 TCCATGGGCTTCAAGACCTTCGGTTTTGCCGGGGGCCGGGTGGACGTATGGGAACCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1104 CIGGIATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAAACGGGATAAAAACG---GG
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                                                                                                                                                                                                                                                                                                                                                                              1; Length 10578;
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9
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                                                                                                                                                                                                                                                                                                                                                                            Score 331.8; DB 1;
Pred. No. 2.7e-87;
0; Mismatches 277;
                                                                    /product="hypothetical protein"
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/db_xref="GI:14524464"
                                                                                                                                                                                                                 .10455)
                                                                                                                                                                                                                                                   complement(9922. .10455)
/gene="SMa2389"
                 protein, tetR family"
/codon_start=1
                                                                                                                                                                                                                 complement(9922.
/gene="SMa2389"
                                                   /transl_table=11
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/note="glimmer
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                                                                                                                                                                                                                                                                                                                                                                                                                524;
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Matches 52
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//protein_id="CAD27226.1"
/db_xref="G1:19338427"
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ILQCTGCDAIKLEGGEBMADTIAFLTKRGVPVMGHTGLMPQOYDTAGGTRSVGHSEHE
TSKIRNDAHAIGGSCRAVVIDGTVEPLAREVTGAMHIPTIGIGASSACDGQYLVSDD
ILGLENDFIPREVKRYDELGKRMSARRRRLVPGGPVATVFRORSTPFRRRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codoi_start=1
/transl_table=11
/transl_table=11
/product="cyrk protein"
/product="cyrk protein"
/protein_id="cb27227.1"
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                    RLE438039 4754 bp DNA linear BCT 09-MAR-2002
Rhizobium leguminosarum bv. phaseoli panB (partial), oxyR and katG
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BLEKREEYLVRRPEDBGKFYPYQRBALREMRLLLLEBCHCFRQALSFCKIGFARPRE
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TPMAKQLVQVSEAVRRSADSSMEGOYVAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen,J.Y.
Molecular Genetics and Physiology of a Catalase-Peroxidase of
Rhizobluum leguminosarum by phaseoli
Thesis (1999) Department of Bology, Imperial College, University
of London, London, United Kingdom,
2 (bases 1 to 4754)
                                                                                                                                                                                                                                                                                                 AJ438039.1 GI:19338426
catalase-peroxidase; katG gene; ketopantoate
catalase-peroxidase; katG gene; ketopantoate
dydroxymethyltransferase; oxyR gene; panB gene.
Rhizobium leguminosarum bv. phaseoli.
Rhizobium leguminosarum bv. phaseoli
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Submitted (01-MAR-2002) Williams H.D., Biological Sciences,
Imperial College, Imperial College Road, London, SW7 2AZ, UKINGDOM
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regulator"
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1. .4754
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RLE438039
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KEYWORDS
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FEATURES

TITLE

SOURCE

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1557 c 1409 9 855 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2036 GGGCAAGCCTTCGACTATGCCGAGGAGTTCAAAAAGCTCCATCTCCACGGCCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           876 CGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGCCGGATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1173 CCTCTTGCCGCCACGCAGATGGGACTTATTATGTCAATCCTGAAGGCCCCGGTGGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 326.2; DB 1;
Pred. No. 1e-85;
0; Mismatches 273;
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64.9%;
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Best Local Similarity 64.9
Matches 516; Conservative
'gene='
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                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein"
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                                                                                                                                                                                                                                                complement(2477. .3175)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:14026361"
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complement(3185.
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AP003010 BA000012
AP003010.2 GI:14026358
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                                                                   2696 GGGGAACC---GTTCCTTATTGGGCCGGAAGGCGGCGCGCAATCGAGGACCAGGGT 2752
                                                                                                                    CTGGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTG 1472
                                                                                                                                              2753 CTCGGCTGGAAGAGCTCGTTCGGCACCGGCGTCGGCAAGGATGCCATCACCGCCGGCCTC 2812
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GYAALYFASKEAGYVTGQTIIVDGGQILPESLEALA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto,S., Watanabe,A., Idesawa,K., Ishikawa,A., Kawashima,K., Kimura,T., Kishida,Y., Kiyokawa,C., Rohara,M., Matsumoto,M., Matsumo,A., Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M., Takeuchi,C., Yamada,M. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
Institute, The First Laboratory for Plant Gene Research; Yana
Institute, The First Laboratory for Plant Gene Research; Yana
Institute, The First Laboratory for Plant Gene Research; Yana
(E-mail: kaneko@kazusa.or.jp, Thizobase/,
URL: http://www.kazusa.or.jp/Thizobase/,
ON Hay 11, 2001 this sequence version replaced gi:11994985.

Location/Qualifiers
I. 340857
/organism="Wesconfizobium loti"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesorhizobium loti (strain:MAFF303099) DNA.
Mesorhizobium loti
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/gene="mll6718"
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/gene="mll6718"
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complement(6. .770)
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Kaneko,T.
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AUTHORS
TITLE
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REFERENCE AUTHORS

MEDLINE JOURNAL

TITLE

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FEATURES

COMMENT

AGFTSYAETVSVYGTEKSFTDCDDTPWSKAFILAAAYASRGVKWRCTSGAGSEILMGFH
EAKSLLYLEABCLCLLQRGWGVQGTQNGGIDGAPITATIPGGVRELMAENLIAVWLDLE
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                            GADTAQALFRDVYDYWIRLPKNSRPRLYLHGLSLGAWNSERSTDMFDVYGDPFQGALW
SGPPYRSGLWRSFTRDRSPGSPAWLPRFRNGSIVREWNQDGYAADPGFVWGPWRIVYL
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SALOPQGEMATLHGREIAGKIRREMVYSLACITGLVVMPATIVAGLELASMMAIA
FALNY IPFTGPLMAT IPFTLEATAGSGSWQLALIVEVGLNY IQFAIGSYLEPFLTGAS
LAISPRAVMFAVFFWSFMWGVPGAFIGVPILLIVVVTWCAHEQSTRMIATLLSGGRQGT
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7907. a8404
7908-"mlr6724"
7907. 8404
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9371. 10375
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/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                   protein"
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complement(11950. .12498)
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10712. 11839
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Length 340857;

Score 323.2; DB 1, Pred. No. 2.4e-84;

21.7%; 64.6%;

Query Match Best Local Similarity

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197579 IGGCCGGCCGATTTCGCCCATACGCCCCCTGTTCATCCGGATGCCTGGCACACGCGA 197638
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                             CACAGCCCTGAATCAAATCCCTGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAG 731
                                                                                                     1092 TGGGAGTCGGACCTG---GTATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAACCGG
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Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S.,
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                                                                                                                                            TGCCCTGCGGATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCC
                                                                                                                                                                                                                                                                                                                  GTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAAT
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 Mismatches
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AL646061 AL646052
AL646061.1 GI:17427701
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratolire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Busset-CEPH, 27 rue Juliette Dodu, 75910 Paris, France, LMMA CNRS URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex.
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MPICPIGAMYNGIVHVEKAEQAGARLIENAVVYKLEVGAGKRIVAAHYKDPKGVDHRV
Arlat, M., Billault, A., Brottier, P., Camus, J.C., Cattolico, L., Cabadler, M., Chlosne, M., Claudel Frenard, C., Cunnac, S., Demange, N., Gaspin, C., Lavie, M., Moisan, A., Robert, C., Saurin, W., Schiex, T., Siquier, P., Thebault, P., Whalen, M., Wincker, P., Levy, M., Genome sequence of the plant pathogen Ralstonia solanacearum Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://sequence.toulouse.inra.fr/R.solanacearum.html.
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by FrameD*
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function="small molecule metabolism"
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Gene name confidence : hypothetical
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/transl_table=11
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predicted by Homology
predicted by FrameD"
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Boucher, C.A.
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PCGKLLADVRQRPTAPPPGKVYRSGGTGRAADGSPKDPAAAPARQPALPLRDPTTAGG
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//note="Product confidence: probable
Gene name confidence: hypothetical
predicted by Codon_usage
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/note="Product confidence : probable
Gene name confidence : hypothetical
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/transl_table=11
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//note="Product confidence : putative
Gene name confidence : hypothetical
predicted by Godon_usage
predicted by Homology
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/note="RS05080"
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1241 8383 1301 8323 1361

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8206 AGCAGCCGCTTCGGCACGCCAAGGCCACCATCACCAGCGGCCTGGAAGTGACC 8147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mycelium-associated Streptomyces reticuli catalase-peroxidase, its gene and regulation by Furs Microbiol. 145, 549-559 (1999)
2 (abses 1 to 2904)
Borovok,I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. I (bases 1 to 2904)
Zou.P.J., Borovok,I., de Orue Lucana,D.O., Mueller,D. and Schrempf,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cpeB gene; Fe regulatory protein; furS gene
8622 GACCTCATGATCCTCACGGGCAACGTCGCGCTGGAGTCGATGGGCTTCAAGACCTTCGGC
                                                             GCCACGCAGATGGGACTTATTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAGATCCT
                                                                                                                                                                                                                        1242 CTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGGCCATGGATGATGAGGAG
                                                                                                                                                                                                                                                                                                      8262 CCAACGTG----GGGCCGGAGCCGGAAGCGGCCGCATCGAAGAACAGGGCCTGGGCTGG
                                                                                                                                                                                                                                                                                                                                                               ACTGTGGCCCTGATCGCGGGGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                               1362 GAAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAGGAGCAGGGACTGGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1422 AAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCC
                                       TTTGCTGGCGGAAGAAGATGACTGGGAGTCGGACCTG---GTATACTGGGGGCCTGAC
                                                                                                                       AACAAGCCTCTTGCAGATAACGGGGATAAAAACG----GGAAACTTCAGAAACCTCTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1997) I. Borovok, Angewandte Genetik der
Mikroorganismen, FB Biologie/Chemie, University of Osnabrueck,
Barbarastrasse 11, Osnabrueck D-49069, FRG
revised by submitter 12-Oct-1998
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/strain="Tu45, described by H.Zahner, University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces reticuli furS and cpeB genes.
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78. .533
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Location/Qualifiers
1. .2904
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Streptomyces reticuli.
Streptomyces reticuli
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78. .82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDHKLIDTODIAALKARIIASGLSVSOLVSTRWASASTFRGSDWRGGANGARIRIADO
KDWEANQPAQLAKVLETLESIQGAFNGAQSGGKKVSLADLIVLAGCAGVEQAAKNAGH
AVEVPFTPGRWDAAQAQTDVESFAVLEPIADGFRNYQKGKYTLPAEALLVDKAQLLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPEMTVLVGGLRVLDTNIGQTRHGVFTQRPESLTNDFFVNLLDMGTEWKATDGRDVF
EGRDRATGALKWTGTRVDLVFGSHSQLRALAEVYGSADAQAKFVRDFVAAWDKVMNLD
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wsnnFfQnLFGYEWELTKSPAGAHQWVAKDAAETIPDAHDPSAKHLPTWLTTDLSLRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPAYEKISRRFYEHPEQFADAFARAWFKLTHRDMGPRARYLGPEVPAEALIWQDPIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3742 GGTGCCGGCCAGCAGCGCTTCGCGCCGCTCAACAGCTGGCCCGACAACGCCAACCTCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACATATGATGGCCGGGGAGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 /function="cell processes; protection responses; detoxification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 198050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="PROBABLE PEROXIDASE/CATALASE (CATA)
OXIDOREDUCTASE PROPEIN"
OXIDOREDUCTASE PROPEIN"
/db_xref="G1:17427787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.7e-82;
0; Mismatches 302; Indels
                                                                                            /product="PROBABLE TRANSMEMBRANE PROTEIN"
/protein_id="Cab14476.1"
/db_xref="GI:17427786"
                                                                                                                                                                                                                                                                                                                                                                                                                                           : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Product confidence : prob
Gene name confidence : putative
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                        /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 314.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence-not_experimental
                                                                                                                                                                                                                                                                                                                     /note="RSc0775; RS05079"
                                                                                                                                                                                                                                                                                                                                        complement(6890. .8257)
                                                                                                                                                                                                                                                                             complement(6890. .8257)
                                                                                                                                                                                                                                                                                                                                                                              /EC_number="1.11.1.6"
                                                                           /transl_table=11
                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                             /gene="katGb"
                                                                                                                                                                                                                                                                                                    /gene="katGb
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Best Local Similarity 63.2%;
Matches 536; Conservative
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DLFILAGNYALENSGFRTFCFGAGREDVWEPDLDVNWGDEKAWLTHRHPEALAKAPLG
ATEWGLIYYNPEGPDHSGEPLSAAAAIRATFCNWGMNDEETVALIAGGHTLGKTHGAG
TENVGPDPEAAPIEEGCAWSTTGSGVGADAITSGLEVVWPOTPOWSNFENLE
KYEWVQTRSFAGAIGFERANDAPELIPDPFDPSKKRKPTMLVTDLTLRFDPEFEKISRR
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MAWHGAGTYRSIDGRGGAGRGQORFAPLNSWPDNVSLDKARRLLWPIKOKYGOKISWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSTSDDIHNTTATGKCPFHQGGHDQSAGAGTTTRDWWPNQLRVD
                                                                                                                                                                                                                                                                             1278
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCACATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTG 1398
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                                                                                                                                            1033 ACGGCCAGAGCATCTCCTGGGCCGACCTGCTGATCCTCACCGGCAATGTCGCCCTGGAGA 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                       CCATGGGATTTAAAACGCTGGGATTTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACC
                                                            1213 GCGAGCTGGAGAACCCGCTCGGCGCGGTCCAGATGGGCCTGATCTACGTCAACCCGGAGG
                                                                                                                                                                                                                                                                                                    1333 GCATGGCGATGAACGACGAGGAGAGCGTCGCCCTGATCGCCGGCGGCCACACTTCGGCA
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                                                                                                                    1105 TG---GTATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATA---AAAACG
                                                                                                                                                                                                                                                                             1219 GCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCAC
                                                                                                                                                                                                                                                                                                                                                          1279 GTATGGCCATGGATGATGAGGAGCACTGTGGCCCTGATCGCGGGGGGCATACATTTGGTA
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E.coll katG gene encoding catalase HP1, complete cds.
M21516
M21516.1 GI:146534
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1 (bases 1 to 2805)
Triggs-Raine, B.L., Doble, B.W., Mulvey, M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 170 (9), 4415-4419 (1988)

    1. '2805'
/organism="Escherichia coli"
/db_xref="taxon:562"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA24040.1"
/db_xref="GI:146535"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
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E.coli (strain K-12) DNA.
Escherichia coli
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FKNLFEYEYELEQSPAGAHQWVAKNAPEIIPDAHDPSKKHRPRMLTTDLSLRFDPIYE
PISRRFYENPEEFADAFARAWYKLTHRDMGPKSLYLGPEVPEETLLWODPLPEREGEL
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NDPDQLAQVLRTLENYQQEFNASSGAKKYSLADLIYLGGAAGVEKAAKEAGFEIQVPF
TPGRYDATEEHTDVESFEALEPTADGFRNYLGKGNRLPAEYLLLDKANLLNLSAPEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:087864"
/translation="MTENHDAIVTDAKSEGSGCPVAHDRALHPTQGGGNRQWWPERL
NLKILAKNPAVANPLDEDFDYAEAFKALDLAAVKRDIAEVLTTSQDWWPADFGNYGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIRNAWHSAGIYR LSDGRGGAGAGORFAPLNSWPDNGNLDKARRLLWPVKKKYGQSI
SWADLLILGGNVALEFMGFKIFGFGGGRADVWEAEEDVYWGPETTWLDDRRYTGDREL
ENPLGAVQMGLIYVNPEGPNGNPDPIAAARDIRETFRRWAMNDEETVALIAGGHTFGK
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ATGEVKWAGSRADLVFGSNSELRALAEVYASDDAKEKFVKDFVAAWHKVMDADRFDLV
                                                                                                                                                               /db_xref="SPTREMBL:087863"
/translation="MTASPTPTTAEELRGAGLRVTAARVALLETVRDGDHLGVEAIAS
                                                                                                                                                                                                  GVRDRVGHISLQAVYEALHALTAAGLVRRIEPAGHPARYEGRVGDNHHHIVCRSCGAV
ADVDCAVGDAPCLIAADDHGFAIDEAEVVYWGLCPDCSTGRSS"
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                                                                                                         protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="catalase/peroxidase"
/protein_id="CAA74698.1"
/db_xref="GI:3758890"
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/gene="cpeB"
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/transl_table=11
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67. .2789
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/gene="cpeB"
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/gene="cpeB"
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13 (19-20-20-1998) Laboratory of Genetics, University of Submission

14 (13-027-1998) Laboratory of Genetics, University of Misconsin, 445 Henry Mall, Madison, WI 53706, USA

11 (13-027-1998) The End of the E. Coll Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHER). The entire sequence was independently determined from E. Coll KN1 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Alianta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG site Nos. unique ID nos. for the genes in the E. Coll Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful dance between the E. Coll content of the database is an ongoing task whose goal is to make the genome sequence more useful dance between the E. Coll content of the database is an ongoing task whose goal is comments to the authors are dependent to the database is an ongoing task whose goal is comments to the authors are dependent of the database is an ongoing task whose goal is comments to the authors are
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(http://www.genetics.wisc.edu). *** The E. coli K12 sequence and
its annotations are periodically updated; this is version M54. No
sequence changes. Annotation updates: updated gene identifications
and products; all new functional assignments courtesy of Monica
Riley; added promoters, protein binding sites, and repeated
sequences described in reference I. The unique numeric identifiers
beginning with a lowercase 'b' assigned to each gene (protein or
RNA-encoding) are now designated as gene synonyms instead of
labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                           1 (bases 1 to 13840)
Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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/db_xref="taxon:83333"
complement(24. .52)
/note="factor Sigma70; promoter metjp3; documented +1 at 4126046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, university of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecol@Genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics University of Misconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459 3 (bases 1 to 13840) Blattner, F.R. Direct Submission
                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
   Escherichia coli K12 MG1655 section 358 of 400 of the complete
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Blattner, F.R.
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Escherichia coli K12
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EMFELLEPIADGFRNYRARLDVSTTESLLIDKAQQLTLTAPEMTALVGGMRVLGGNFD
GSKNGVFTDRVGVLSNDFFVNLLDMRYEWRATDESKELFEGRDRETGEVKFTASRADL
VFGSNSVLRAVAEVYASSDAHEKFVKDFVAAWVKVMNLDRFDLL"
625 a 721 c 805 g 654 t
About 89 minutes. on K-12 map.
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FLNDPQAFNEAFARAWFKLTHRDMGPKSRYIGPEVPKEDLIWQDPLPQPIYNPTEQDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 TCTAACCCACTGGGTGAGGACTTTGACTACCGCAAAGAATTCAGCAAATTAGATTACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCTGAAAAAAGATCTGAAAGCCCTGTTGACAGAATCTCAACCGTGGTGGCCAGCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGGTCTGGAAGTAGTCTGGAC 1101
                                                                                                                                                                                                                                                                     20.5%;
62.1%;
                                                                                                                                                                                                                                                                                                                             499; Conservative
                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                Matches
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/translation-"MSFFHASQRDALNQSLAEVQGQINVSFEFFPPRTSEMEQTLWNS
IDRLSSLKPKFVSVTYGANSGERDRTHSIIKGIKDRTGLEAAPHLTCIDATPDBLKTI
IDRLSSLKPKFVSTYGANSGERDRTHSIIKGIKDRTGLEAAPHLTCIDATPDBLKSTADYSWNNGIHIVALKROLPPESKSAQADLLNLKRKVDAGANRAITQFFFDVESYLRFRDRCVSAGIDVEIIFGILPVSNFK
QAKKRADMTNRIPARIAQMFGCLDDDAETRKLVGANIAMDMVKILSREGVKDFHFYT
LNRAEMSYAICHTLGVRPGL"
                     HVISANKLAGASDSNKYRQIHDAFEKTGRHWLYNATVGAGLPINHTVRDLIDSGDTIL
SIGGIFEGGIEDPORDLSGKOVRRKLVILAR
SIGGIFEGGIEDPORVRESLYDAMGGGSTEDPRORDLSGKOVMKLVILAR
SIGGYNIEPDOVRVESLYPAHGEGGSIDHFFENGDELNBOMYQRLEAREMGIVLRYVA
RFDANGKARVGVEAVREDHPLASLLPCDNVFAIESRWYRDNPLVIRGPGAGRDVYTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  684 TCAAATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAG 743
GLDASRALAFFNDEAVEQDEESLFLWMRAHPYDDLVVLDVTASQQLADQYLDFASHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="enzyme; Central intermediary metabolism: Pool
                                                                                                                                              3898...3931
/note="REP (repetitive extragenic palindromic) element;
contains 1 REP sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   804 TATGGTCATTATGGTCCTTTCTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGGCAGTTACGCCGGTCTGTTATTCGTATGGCCTGGCACGGCGCGCGGGACTTACCGT
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                                                                                                                                                                                                     councains in the sequence...
4086. 4086

/note="factor Sigma70; promoter metf; documented +1 at4130126"
4084. 4003

/note="central position to metf promoter: -8"
/bound_molety="MetJ documented site"
4098. 4107

/note="central position to metf promoter:6"
/bound_molety="MetJ documented site"
4098. 4107

/note="central position to predicted promoter:6"
/bound_molety="MetJ predicted site"
4114. 4123

/note="central position to metf promoter:6"
/bound_molety="MetJ predicted site"
/fore="central position to metf promoter:2"
/bound_molety="MetJ documented site"
/gene="metf"
/gene="metff"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="5,10-methylenetetrahydrofolate reductase"
/protein_id="AAC76923.1"
/db_xref="G1:1790377"
                                                                                                                                                                                                                                               promoter metF; documented +1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multipurpose conversions"
/note="0296; 100 pct identical amino acid sequence
equal length to METE_ECOLI SW: P00394; CG Site No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 305.4; DB 1; Length 13840;
Pred. No. 2.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5317. .5330
/note="central position to katG promoter: -39"
/bound_molety="OxyR documented site"
/bound_molety="S354
/note="factor Sigma70; promoter katG; document
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 301; Indels
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4167. .5057
                                                                                                                   IQSDINRLAQLL"
3898. 3931
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62.1%;
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/gene="metF"
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/gene="katG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at4131392"
5386. .756
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Best Local
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Matches
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ALAGVSRVTIMSDVAGVYSADPRKVKDACLLPLLRLDEASELARLAAPVLHARTLQPV
SGSETDLQLRCSYTPDQGSTR ERVLAASGTGARITYSBIDDVCLIEFQVPASQDFRLAH
LYLDQLIKRAQVRPLAVGYNTRYDRULLGFCYTSEVADSALKILDEAGLPGELRLAQGLA
LYJAMYGAGYTRNPLGHRFWQQLGCYTSEVADSALKILDEAGLPGELRLAQGLA
SYFRARKRIGLVLFGKGNIGSRWLELFAREQSTLSARTGFFEVLAGVVDSRRSLLSYD
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MVVSAAGSTTNQLINWLKLSQTDRLSAHQVQQTLRRYQCDLISGLLPAEEADSLISAF
VSDLERLAALLDSGINDAVYAEVVGHGEVWSARLMSAVLNQQGLPAAWLDAREFLRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSYRLEDSLAKRGCYRVLFVDQGDEGALRAALAEKPKLVLVESPSWPLIKVDJTAKLC
HLAREYGAVSVVDNTFLSPALONPLALGADLVLHSCTKYLNGHSDVVAGVVTAKDPDV
VTELAWWANNIGVTGGAFDSYLLLRGIRTLVPRMELAQRNAQAIVKYLQTOPLVKKLY
HPSLPRNGGHETAARQOKGFGAMLSFELDGDEQTLRRFLGGLSLFTLAESLGGVESLI
SHAATWTHAGNAPEARAAGISETLLRISTGIEDGEDLIADLENGFRAANKG"
1386. 3818
/gene="metl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'translation-"MTRKQATIAVRSGLNDDEQYGCVVPPIHLSSTYNFTGFNEPRAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYSRRGNPTRDVVQRALAELEGGAGAVLTNTGMSAIHLVTTVFLKPGDLLVAPHDCYG
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                               at
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/note="0810; 100 pct identical to AK2H_ECOLI SW:
P00562;bifunctional enzyme; CG Site.No. 506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"aspartokinase II and homoserine dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="enzyme; Amino acid biosynthesis: Methionine"
Anote="0386; CG Site No. 515"
/codon_start=1
                       /note="factor Sigma70; promoter metjp2; documented +1 4126109"
                                                                                                         Ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mote="central position to predicted promoter: -132"
/hound_molety="MetJ predicted site"
complement(169. 178)
/hound_molety="MetJ predicted site"
/hound_molety="MetJ predicted site"
complement(185. 194)
/hote="central position to predicted promoter: -147"
/hote="central position to predicted promoter: -163"
/hound_molety="MetJ predicted site"
                                                                                                                                                                             /note="central position to metB promoter: -58"
/bound_molety="MetJ documented site"
complement(138. .147)
/note="central position to predicted promoter: -116"
/bound_molety="MetJ predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(115. .144)
/note="factor Sigma70; promoter metJpl; documented
4126138"
                                                                                                                                                                                                                                                                                                                                                                                     148. .157 /
/note="central position to metB promoter: -34"
/bound_moiety="MetJ documented site"
                                                                                                                                                                                                                                                                                                                                note="central position to metB promoter: -42'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="cystathionine gamma-synthase"/protein_id="AAC76921.1"
/db_xref="G1:1790375"
                                                                                                                                                                                                                                                                                                                                                             bound_moiety="MetJ documented site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC76922.1"
/db_xref="G1:1790376"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /EC_number="2.7.2.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/trans1_table=11
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1386. 3819
             complement (88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="b3939"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223. .1383
/gene="metB"
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/gene="metB"
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/gene="metL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at4126216"
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This sequence was determined as part of the E. coll Genome Project (Frederick R. Blattner, director) at the University of Misconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. A preliminary report was presented at the Small Genomes meeting, March 28-30 1993, Paris, France. The entire sequence was independently determined from E. coll MG1655, overlaps and conflicts with other sequence determinations are annotated. The start of this entry overlaps the end of the entry ECOUW85U (M87049) by the three bases of an ECORI half-site. Data kindly submitted in Guy Plunkett III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /traislation="MIPLLAPAAWSGTGKTTLLKKLIPALCARGIRPGLIKHTHHDWD
VDKFGKDSYELRKAGAAQTIVASQQRWALWTETPDEEELDLQFLASRMDTSKLDLILV
BGFKHBEIAKIVLFRDGAGHRPEELVIDRHVIAVASDVPLNLDVALLDINDVEGLADF
VVEWMQRQNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="This sequence comprises the following lambda clones: EC21-16, EC27-1225, EC27-649, EC19-119, EC23A58, EC27-267, EC18-126. Ml3mpl9 or Janus vectors were used for subcloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Eco RI half-site is 3bp overlap with end of M87049
                               DNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2459. 2483
/nocle="putative"
2504. 2540
/standard_name="REP; repetitive extragenic palindromic
Plunkett,G. III, Burland,V., Daniels,D.L. and Blattner,F.R. Analysis of the Escherichia coll genome. III. DNA sequence region from 8.2 to 89.2 minutes Nucleic Acids Res. 21 (15), 3391-3398 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="corresponds to lambda clone EC21-16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains 1 REP sequence"
complement(2546...3058)
/standard_name="ORF £170"
/note="matches PS00017: ATP_GTP_A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'RNA"
23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Escherichia coli"/strain="K-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAB02991.1"
/db_xref="G1:304962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="23S ribosomal'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ecoli@genetics.wisc.edu 608-263-7459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub_strain="MG1655"
/db_xref="taxon:562"
/tissue_lib="lambda"
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/note="putative"
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University of Wisconsin
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2157. .2276
/gene="rrfA"
2157. .2276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 Tibosomal RNA; 5,10 methylenetetrahydrofolate reductase; 508 ribosomal RNA; 5,10 methylenetetrahydrofolate reductase; 508 ribosomal protein L31; 55 ribosomal RNA; 6-phosphofructokinase; CDP-d419/ceride hydrolase; DNA polymerase 1; L-fhamnose isomerase; Spot 42 RNA; aspartokinase I; Ichomoserine; attP2II; catalase HPI; catalase hydroperoxidase I; Ichomoserine; ratP2II; catalase HPI; gene; cystathionine; cytR gene; dehygrogenase II; dsbA gene; extragenic palindromic element; idhD gene; idoB gene; fdoG gene; fdoH gene; fdoI gene; formate dehydrogenase-0 alpha subunit; formate dehydrogenase-0 beta subunit; formate dehydrogenase-0 gamma; gamma-synthase; glA gene; metB gene; metB gene; metF gene; metF gene; metJ gene; metF gene; metB gene; perlplasmic sulphate binding protein; pfkA gene; priA gene; rhaD gene; rhaD gene; rhaR gene; rhaR gene; rhaR gene; rhamnose permease; rhamnolose per
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                                                  TACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAA 1043
                                                                                                                                                                                                                                          6022 GCGAAAGCACCGCTGGGTGCAACCGAGATGGGTTAACCTTAACCCGGAAGGCCCG 6081
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                                                                                                                                                                                                                                                                         5902 AACTCCGGCTTCCGTACCTTCGGTTTTGGTGCCGGTCGTGAAGACGTCTGGGAATCCGGAT
                                                                                                                                                                                                                                                                                                                                               CTGGTATACTGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATAAAAACGGGAAA
                         TGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAA
                                                                                                                                                                5962 CTGGATGTTAACTGGGGTGATGAAAAGCCTGGCTGACTCACCGTCATCCGGAAGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1224 GGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATG
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E. coli chromosomal region from 87.2 to 89.2 minutes.
L19201
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ECOUW87
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GVERFIKDENDAKKGEHAYDWILSYQNFDKGFFNSREQMQWTFDNGAPDLNIKFGQK
GVERFIKDENDAKKGEHAYDWILSYQNFDKGFFNSNERFEGANKSPVEATLRF
AFGGSFSTILDVAPAEVGKFGFGEGGFTFNGDGSSLSNLDIEGKVEDIYLQLEPWNKY
TAKSFTIDSLARLEEKKFPVGESEGKFFNQINIINHGEDVAQIDAFVAKTRLDRVKDKD
               FSFFCPHCYQFEEVLHISDNVKKKLPEGVKMTKYHVNFWGGDLGKDLTQAWAVAMALG
VEDKVTVPLFEGVQKTQTIRSASDIRDVFINAGIKGEEYDAAMNSFVVKSLVAQQEKA
translation="MKKIWLALAGLVLAFSASAAQYEDGKQYTTLEKPVAGAPQVLEF"
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                                                                                                                                       /note-"in X63186, 'a' in M77746, 'g' in this sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           684 TCAAATCCCTGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAG
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                                                     AADVQLRGVPAMEVNGKYQLNPQGMDTSNMDVFVQQYADTVKYLSEKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 305.4; DB 1; Length 96484;
Pred. No. 3.7e-79;
0; Mismatches 301; Indels 3;
                                                                                                                                                                                                     'tcacgggc' in this sequence"
                                                                                                                                                                                                                                            5729. .5756 //
/note="promoter matrix score of 58; putative"
                                                                                                                                                                                                                                                                       5797, .7269
/standard_name="ORF_0490"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAB02996.1"
/db_xref="G1:304967"
                                                                                                                                                        /replace="ata"
5718 .5725
//note="in x63186, 'replace="cacgg"
5729 .5756
                                                                             5703. .5731
/note="putative"
5714
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llarity 62.1%;
Conservative
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/transl_table=11
/brotein_id="aAB02993.1"
/db_xref="G1:M4964"
/translation='MKCKRLNEVIELLQPAWQKEPDLNLLQFLQKLAKESGFDGELAD
LIDDILIYHLKMRDSAKDAVIPGLQKDYEEDFKTALLRARGVIKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAB02994.1"
/db_xref="GI:304965"
/translation="MNNSAFTFQTLHPDTIMDALFEHGIRVDSGLTPLNSYENRVYQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDEDRRREVVKFYRPERWTADQILEEHQFALQLVNDEVPVAAPVAFWGGTLLNHQGFY SPAFPENGERGREADNIDQMENVGRYLSCHMGFKQLF-REDATLENBLEFRLEF EDATLIPENGERATGERGAFTER EDATLIPESGERAAFERATDELIAAVTAHWREDFTVLRLHGDGHAGNILWRDGFWFVDL DDARNGPAVQDLWMLLNGDKAEQRWQLETIIEAYEEFSEFDTAEIGLIEPLRAMRLVY
                                                                                                                                                                                                       /translation="milmttigyvlaggkarrmggydkgllelngkplwqhyadalm
Tqlshvyvnanrhqelyqasglkyledsladypgplagmlsymqqeagewflepedd
pylpplaarlnhqrkdapyvwyhdgerdhptialynralepilleylqagerrymyf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLAWLMRRWADPAFPKNFPWLTGEDYWLRQTATFIEQAKVLQEPPLQLTPMY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126. .6322
'note="corresponds to X63186; ECOPPFA(1. .2192)'
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                                                                                                                                                                                                                                                                                                                                                                    /note="promoter matrix score of 48; putative" complement(3691. 3720)
/note="promoter matrix score of 66; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="promoter matrix score of 69; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="in X63186; absent in this sequence"/replace="c" 4883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="in X63186; absent in this sequence"
                                                                               /function="biosynthesis of molybdopterin"
/note="CG Site No. 921"
                                                                                                                                                                                                                                                           MRLAGGHAVDPSDHKDAFVNVNTPEELARWQEKR complement(3642..3668)

finde="55% match to consensus; resembles flhc/flhb-regulated promoter; putative" 3653..3680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3743. .3898
/note="predicted bend of 84.96 degrees"
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/replace="
misc_difference 4792^4793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1056. .5042
/standard_name="ORF_0328"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAB02995.1"
/db_xref="GI:304966"
                                                                                                                                           /transl_table=11
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/db_xref="G1:304963"
                                                                                                                                                                                                                                                                                                                                                                                                                                    3709. .3978
/standard_name="ORF_089"
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/transl_table=11
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4865^4866
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gene="dsbA
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misc_difference 4481
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/product="putative regulator"
//product="butative regulator"
//db xref="c1:13164200"
//translation="MIPFNAPPVVGTELDYMOSAMGSGKLGGDGGFTRRCOOWLEORE
GSAKVILIPESCTASLEMAALLILDIOGEODYINEYSTFVSTAMAFVLIRGARIVEYDORP
GSAKVILIPESCATSLEMAALLILDIOGEODYINEYSTFVSTAMAFVLIRGARIVEYDORP
GYGNYTHUNDETLIEAALIPETRYIVPVHYAGVACEMDTIMALAKHNLEYVEDAAQGYWST
YKGRALGTIGHIGCFSFHETKNYTAGGEGGATLINDKALIERAEIIREKGTNRSQFFR
GOVDKTYMADIGSSTAMSDLOAAXIMADLEAADHINGONTAGAR
IELPSTPDGCLQNAHMEYIKLRDIGDRSALINFLKRAEIMAVFHYIPLHGCFAGGERFG
EFHGEDRYTTKESERLLRLPLFYNLSPVNQRTVIATLLNYFS"
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AQETDIPALRQLASAAFAQSRFRAPWYAPDASSRFYAQWIENAVRGTFDHQCLILRAA
SGDIRGYVSLRELNATDARIGLLAGRGAGELMQTALNWAYARGKTTLRVATQMGNTA
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LPTLSRLTEKRDITREVVKSLKFVLPAVAAASFTVWLLRDFAIWLLLSNKFTAMRDLF
AWQLVGDVLKVGAYVFGYLVIAKASLRFYILAEVSQFTLLMVFAHWLIPTHGALGAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSLAKASLWTAASTLVKIGAGLLVGKLLAVSFGPAGLGLAANFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLITVLGVLAGAGIFNGVTKYVAQYHDNPQQLRRVVGTSSAMVLGFSTLMALVFVLAA
APISLGLFGNHDYQGLVRLVALVQMGIAWGNLLLALWKGFRDAAGNALSLIVGSLIGV
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                                                                                                                                                                                                                                                                                               /gene="ECs4723"
/note="similar to WECD_ECOLI gi|1790225 percent identity 98 in 181 as (Conserved in E.coli K-12)"
/codon_start=1 /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"similar to WECE_ECOLI gi[2367285 percent identity 99 in 376 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to WZXE_ECOLI g1|1790227 percent identity 98 in 416 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="N-terminal part (1-62 in 359 aa) is similar to YIFM_1_ECOLI gil2367286 percent identity 96 in 62 aa, C-terminal part (156-359 in 359 aa) is similar to YIFM_2_ECOLI gil2367287 percent identity 96 in 204 aa /codon_start=1
                                                                           1. .318703
/organism="Escherichia coli O157:H7"
/strain="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="BAB38146.1"
/db_xref="GI:13364199"
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                                                                                                                                                         /sub_strain="RIMD 0509952"
/db_xref="taxon:83334"
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653. .1783
/gené="ECs4724"
653. .1783
                       genome project.
Location/Qualifiers
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/gene="ECs4723"
103. .648
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1785. .3035
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/gene="ECs4725"
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/qene="ECs4726"
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/gene="ECs4726"
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Fax:81-6-6879-2047)
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                       COMMENT
                                                                     96284 CACGGTGCCG---GTCCGACATCAAATGTAGGTCCTGATCCAGAAGCTGCACCGATTGAA 96340
                                                                                                                                                               1403
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Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7 Genes Genet. Syst. 74 (5), 227-239 (1999)
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (strain:0157:H7, sub_strain:RIMD 0509952)
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Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 (bases 1 to 318703)
Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
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Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
20557356
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Escherichia.
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Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
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Haysshi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
Shinagawa,H.
                       CATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAG
                                                                                                                         1404 GAGCAGGGACTGGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                       AP002567 318703 bp DNA linear BCT 07-MP
Escherichia coli 0157:H7 DNA, complete genome, section 18/20.
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                                                                                                                                                                                                                                                                          1464 AGTGGCCTGGAAGGAGCCTGGTC 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 0157:H7
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AP002567.1 GI:13364198
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864 ACATATGACGCGGGGGGGGCGCCAGTGGTCGGCACGTTTGAACGCTGAACAGC 923
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAA 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1044 TCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTCGGAC 1103
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                                                                                                                                             744 GCTCTGAAAAAAAAATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGAT
                                                                                                                                                                                                       804 TATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGG
                                                                                                                                                                                                                                                                                                                                                                  TGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAA
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Aspergillus nidulans.
Aspergillus nidulans.
Bukaryota; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
1. (bases 1 to 3018)
Scherer.M.
Thesis (2001) Department of Microbiology,
                                      684 TCAAATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAG
Gaps
3;
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  Indels
Mismatches 302;
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AJ305225.1 GT:15384982
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  Conservative
  Matches 498;
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ANI305225
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KIGITAAAGIINFVVLTAALSGCNSGMYSCGRMLYALAKNRQLPAAMAKVSRHGVPVA
GVAVSIAILLIGSCLNYIIPNPQRVFVYVYSASVLPGMYPWFVILISQLRFRRAHKAA
IASHPFRSILFPWANYVTMAFLICVLIGMYFNEDTRWSLFVGIIFMLAVTAIYKVFGL
                                                                           /translation="myvilhydgddphhnryvlrefndalatgeharefwydgndd
GLSDSCPALSYQFFPGKKSLAEAVIAKAANRQORFFFHGGFNPTLMLALLSGGIRPS
GLSDSCPALSYQFFPGKKSLAEAVIAKAANRQORFFFHGGFNPTLMLALLSGGIRPS
GPYMHYMGADLYELSSGLRYKLFYPLARLAOKRYGCYFATRGOLSFFATHFRYNGEL
LYFPTRMDALNTMANDRQREGKMTILYGNSGDRSNEHIAALLRAYBQFGGTVKVVVV
MGYPPHWEAY IEBYNGAGLEFESEBNLOVLSEKLEFDAYLTLLRQCALGYFIFARQOG
IGTLCLLIQAGIPCVLNRENFWQDMTEQHLFYTFDDLNEDIYREAQRQLASYDKN
TIAFFSPNYLGGWQRALAIAAGEVA"
4108. 5460
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naekhitieenaevrelinaaefkyadgisvvrsvrkkypoaqvsryagadiweelma
rackegtypeliggrevladtaaktenomnvnivgsodgifkpedroalferihasg
aqivtyamgsproelembocalvhedalimgvggitdyftghyrrabkingticeemi
yrllsopsrikrolelrylemhytghl"
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VLATAITGCTVFVFTRKSWAGRHLFLEPPTGSFRVYAHKYWERPPEGYLTANSYWFWWAN
VGISBITAIGVYWFPERAQWIPALIAVALVALANIAAVRLYGEIEFWFAHKVYT
ITVMYVIGLGVIFFGFGNGGQSIGFSNLTEHGGFFAGGWKGFLTALCIVVASYQGVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLIQNYDNIDFOGLAPIYRDFYYFIPSWLWPCRPSMYLNSANYFTWEVLNNHSCLAIS
PTLIGSLYVWGGALFIPLGAIVYGLIIKWFDWLYELGNRETNRYKAALLHSFCFGAIF
NMIYLAREGLDSFYSRYVFFIYVFGACLMIAKLLYWLFESAGLIHKRTKSSLRTQYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"msllopsglevvwllctlfiatifweefrrvrenpnvffsllfl
LTFFFGFPLTSVLVPRFDVGVaPPEILLOALLSAGCFYAVYYVTKTRLRKRVADVPR
RPLFTWNRVETNLTWVILMGIALVSVGIFFMHNGFLLFRLNSYSQIFSSEVSGVALKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFYFFIPAMLVVYFLRQDSKAWLFFLVSTVAFGLLTYMIVGGTRANII1AFAIFLFIG
IIRGWISLMMLAAAGVLGIVGMFWLALKRYGMNVSGDEAFYTFLYLTRDTFSPWENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to YIFK_ECOLI gi[2367290 percent identity 98 in 461 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gi|2367289 percent identity coli K-12)"
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19 in 450 aa (Conserved in E.coli K-12)"
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                                                                                                                                                                                                                                                                                                                                                                                                             /product-"TDP-Fuc4Nac:lipidII transferase"
/protein_id="BaB38150.1"
/db_xref="GI:l3364203"
                     /product-"hypothetical protein"
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/db_xref-"G1:13364202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to WECG_ECOLI
98 in 246 aa (Conserved in E.
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/protein_id="BAB38152.1"
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/db_xref="GI:13364204"
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6394. 777
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/gene="ECs4728"
5463. .6203
/gene="ECs4728"
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/gene="ECs4729"
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/gene="ECs4727"
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173573

1283

173633

1403

1463

AUTHORS

Score 303.8; DB 1; Length 318703; Pred. No. 1.5e-78;

20.4%;

Query Match Best Local Similarity

1345

1063

1165

1405

1465

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DNA linear BCT 21-MAR-2001
genome, contig 3 of 3, section 244
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homologous to E. coli K-12 MG1655"
complement(253. .861)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 10667)
Pernah. N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K.,
Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
Welch,R.A. and Blattner,F.R.
                                                                                                           1004 CGACAACCCGCTTGCGGGCATCACATGGGTCTTATTATGTTAATCCAGAAGGACCCCAA
                                                                                                                                                                                                                                                                          1124 CATGAATGATGAGGAGACTGTTGCCCTGATTGCTGGTGGACACACGTTCGGAAAGACGCA
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    CTGGGGGCCTGACAACAA-----GCCTCTTGCAGATAACCGGGATAAAACGGGAAACT
                                                                                                                                                                                                            1064 CAAGAACCCCGACCCGGTTCTCGCGGCCAAGGATATCCGCATCACCTTTGGTCGAATGGC
                                                                                                                                                                                                                                                  944 CTTCTGGGGAGGCGAGAAGGAATGGTTGGGTAATGATGTCCCGCTACTTGAACGGAGAACT
                                                                                                                                                                   TGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGGC
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Submitted (22-OCT-2000) Laboratory of Genetics, Ur
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
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Escherichia coli 0157:H7 EDL933
of 290.
AE005625 AE005174
AE005625.1 GI:12518851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1301 CGGTCTGGAGGTGATCTGGACCA 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /serotype="0157:H7"
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AE005625
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JOURNAL
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KOKORNDAGOSTDKRVSLADLIVLAGAASLEKAARDAGHVSVSFTPCRTDAYDGOTD
VDSFNNLEPTADGFRYGRGTPRVLTEDFLIDKAQLLNLSPPELTVLIGGLRVLNNNY
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                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAC59821.1"
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/translation="MGSNECPYSRQNANIGGGGQNNRDWWPDDLKLNILRQHNSVSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDGRGGGGGGQQRFAPLNSWPDNVSLDKARRLLWPIKQKYGSKISWADLLILAGNVAL
ESMGFKTFGFAGGRSDTWEADQSVFWGGEKEWLGNDVRYLNGELDNPLAASHMGLIYV
NPEGPNKNPDPVLAAKDIRITFGRMAMNDEETVALIAGGHTFGKTHGAGPATHLGKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGAGIELQGLGWESGFESGTGRHAITSGLEVIWTKTPTKWSNOFFEYLFKYDWELFKS
PAGAHQYVAKGVEPFIPDPFDPSIKHPPRMLTTDLSLRYDPEYEKISRRFLENPDQFA
DAFARAWFKLTHRDVGPRVLYQGPEVPSEVLIWQDPVPPLDHPVIDNDIATLKKAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDKGFDYTAAFNSLDYFGLKRDLEALMTDSQDWWPADFGHYGGLFIRMAWHSAGTYRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   752 AAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     812 TTATGGTCCTTTCTTTATTCGTATGCCTTGGCACGGTGCCGGAACATACAGGACATATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    872 TGGCCGGGGAGGCGCCAGTGGTGGTCACCATTTTGAACCGCTGAACAGCTGGCCGGA
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                   2 (bases 1 to 3018)
Scherer,M.
Direct Submission
Submitted (25-JAN-2001) Scherer M., Biochemistry,
Max-Planck-Institut fuer Terrestrische Mikrobiologie,
Karl-von Frisch-Str., 35043 Marburg, GERMANY
revised by author 10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 303.4; DB 8; Length
Pred. No. 6.2e-79;
0; Mismatches 326; Indels
Philipps-Universitaet-Marburg, Marburg, Germany
2 (bases 1 to 3018)
                                                                                                                                                                                                            nidulans
                                                                                                                                                                                                                                                                                                                                                                        /product="catalase-peroxidase"
                                                                                                                                                                                                     /organism="Aspergillus
/db_xref="taxon:5072"
                                                                                                                                                                                                                                                                                                                                /EC_number="1.11.1.6"
                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                              393. .2612
/gene="cpeA"
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/gene="cpeA"
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ilarity 61.2%;
Conservative
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Matches
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TITLE
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                                                                                                                                                                                                                                                                                                                                                              /db_xref="G1:1218852"
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SYSTHGMLYMRKRPVFEAVGPVYTPLKQMIAHGEKGKYVVRRVEGGLSVEQQK
LAQTAKRYLGKPDRSFSWSDDRQYCSEVWRKYYQNALGMRYGEQQKLKEFDLSNPLV
QAKLKERYGKNIPLEETVVSPQAVFDAPQLTTVAKEWPLFSW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="enzyme; Amino acid biosynthesis: Methionine" //note="Residues 1 to 386 of 386 are 99.48 pct identical to residues 1 to 386 of 386 from Escherichia coli K-12 Strain MG1655: 83339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MTRKQATIAVRSGLNDDEQYGCVVPPIHLSSTYNFTGFNEPRAH
DSYRRONPTRDVVQRALAELEGGAGATLATURCARSAIHUYTPTERPEDLAPHIDCYG
GSYRLFDSLAKRGCYRVLFVDGDEGALRAALAENPKLVLVESPSNPLIKPUCYG
GSYRLFDSLAKRGCYRVLFVDGDEGALRAALAENPKLVLVESPSNPLIKPUCYG
HLAREVGAVVDNTFLSPALQNPLALGADLVLHSCTKYLNGHSDVVAGVVIAKDPV
TYELAWWANTGYTGGAFDSYLLLRGFHTVPRPARALARAIVKLYGTQPLVKKLY
HPSLEBNGGHEIAARQCKGFGAMLGSFLELDGDEGTLRRFLGGISLFTLAESLGGVESLI
SHAATWTHAGMAPEARAAAGISETLLRISTGIEDGEDLIADLENGFRAANKG
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/note="Residues 1 to 810 of 810 are 99.87 pct identical to
residues 1 to 810 of 810 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AaG59141:1"
/db_xref="G1:12518855"
/db_xref="G1:12518855"
/db_xref="G1:12518855"
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/note="Residues 1 to 202 of 202 are 97.52 pct identical to
residues 1 to 202 of 202 from Escherichia coli K-12 Strain
MG1655: B3937"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="regulator; Amino acid biosynthesis: Methionine" Anche="Residues 1 to 105 of 105 are 100.00 pct identical to residues 1 to 105 of 105 from Escherichia coll K-12 strain MG1655: B3938"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAEWSGEVISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRR
QVNNLRHATNSELLCEAFLHAFTGQPLPDDADLRKERSDEIPEAAKEIMREMGINPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="repressor of all met genes but metF"
/protein_id="AAG59139.1"
/db_xref="GI:12518853"
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/product="cystathlonine gamma-synthase"
/protein_id="AAG59140.1"
/db_xref="G1:1218888"
                                                                                                                                                                                                                                                                          /transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAG59138.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(921. .1238)
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                                                             complement(253. .861)
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residues 1 to 810 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="metB"
/note="Z5494"
1515. .2675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="25493"
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/gene="metL"
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/gene="metB"
                                                                                          /gene="yiix"
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/gene="metL"
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CDS

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multipurpose conversions of intermed. met'm" hote-"Residues 1 to 296 of 296 are 99.66 pct identical to residues 1 to 296 of 296 from Escherichia coli K-12 Strain MG1655. /product="5,10-methylenetetrahydrofolate reductase"
/brotein_id="AAG59142.1"
/db_xref="G1:1251886"
/translation="MRFHASORDALNQSLAEVOGQINVSFEFFPPPRTSEMEOTLWNS
IDRLSSLKPKFVSVTYGANSGERDRTHSIIKGIKDRTGLEAAPHLTCIDATPDELRTI
SAQADLLINLKRKVDAGANRATTQFFDVESYLRFRDRCVSAGIDVEIIPGILPVSNFK
QAKKRPADMTNRIPARGILPGEDDDAETRKLVGANIAMDMYKILSREGVKDFFTYI
INRAEMSYRACHTLGVRPGL" /function="orf; Unknown function" % Actor="Residues 1 to 312 of 312 are 98.71 pct identical to residues 1 to 312 of 312 from Escherichia coli K-12 Strain MG1655: B3943" LVAMVGAGVTRNPLHCHRFWQQLKGQPVEFTWQSDDGISLVAVLRTGPTESLIQGLHQ SVFRAEKRIGLVLFCKGNIGSRWLELFAREQSTLSARTGFEFVLAGVVDSRRSLLSYD GLDASRALAFFNDEAVEQDEESLFLWMRAHPYDDLVVLDVTASQQLADQYLDFASHGF HVISANKLAGASDSNKYRQIHDAFEKTGRHWLYNATVGAGLPINHTVRDLIDSGDTIL STGTIFSGTENDLSGKVPFTELTDDQAWQGLTEPDPRNDLSGKVVMKLVILAR STGTINGTEDDVKWSELVPAHGEGSIDHFFENGDELNEOWYRLEAREWGIVLRYVA RFDANGKARVGVEAVREDHPLASLLPCDNVFALESRWYRDNPLVIRGPGAGRDVYAGA /function="enzyme; Protection responses: Detoxification" forte="Residues 1 to 726 of 726 are 99.86 pct identical to residues 1 to 726 of 726 from Escherichia coli K-12 Strain MG1655: B3942" ATEMGLIYVNPEGPDHSGEPLSAAAAIRATFCNMGMNDEETVALLAGGHTLGKTHGAG PTSNVXPDPEAAPIEEQGLGWASTYGSGVGADAITSGLEVVWTQTPTQWSNYFFENLF KYEWVQTRSPAGAIQFEAVDAPEIIPDPFDPSKKRRPTWLVTDLTLRFDPEFEKISRR ALPVLEKIOKESGKASLADIIVLAGVVGVEKAASAAGLSIHVPFAPGRVDARODOTDI EMFELLEPIADGFRNYRARLDVSTTESLLIDKAQQLTLTAPEMTALVGGMRVLGANFD GSKNGVFTDRVGVLSNDFFVNLLDMRYEWKATDESKELFEGRDRETGEVKYTASRADL ALAGVSRVTIWSDVAGVYSADPRKVKDACLLPLLRLDEASELARLAAPVLHARTLQPV SGSEIDLQLRCSYTPDQGSTRIERVLASGTGARIVTSHDDVCLIEFQVPTSQDFKLAH KEIDQILKRAQVRPLAVGVHNDRQLLQFCYTSEVADSALKILDEAGLPGELRLRQGLA FLINDPQAFNEAFARAWFKLTHRDMGPKSRYIGPEVPKEDLIWQDPLPQPIYNPTEQDI IDLKFAIADSGLSVSELVSVAWASASTFRGGDKRGGANGARLALMPQRDWDVNAAAVR /translation="MSTSDDIHNTTATGKCPFHQGGHDQSAGAGTTTRDWWPNQLRVD LLNQHSNRSNPLGEDFDYRKEFSKLDYYGLKKDLKALLTESQPWWPADWGSYAGLFIR MAWHGAGTYRSIDGRGGAGRGQQRFAPLNSWPDNVSLDKARRLLWPIKQKYGQKISWA DLFILAGNVALENSGFRTFGFGAGREDVWEPDLDVNWGDEKAWLTHRHPEALAKAPLG /function="enzyme; Central intermediary metabolism: Pool, VFGSNSVLRAVAEVYASSDAHEKFVKDFVAAWVKVMNLDRFDLL 8919. .9857 /product="catalase; hydroperoxidase HPI(I)" /codon_start=1 /transl_table=11 /product="orf, hypothetical protein" /protein_id="AAG59144.1" /protein_id="AAG59143.1" /db_xref="GI:12518857" /transl_table=11 /transl_table=11 /note="25497" 6678. .8858 /gene="katG" /codon_start=1 /codon_start=1 /note="Z5496" 5459. .6349 6678. .8858 /gene="katG" **TOSDINRLAQLL"** 8919. .9857 /gene="yijE" 5459. .6349 /gene="metF" 5459. .6349 /gene="metF"

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/transl_table=11
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/gene="katG"
/codon_start=1
                                                                                                               crescentus.
                                                                                      GI:2605729
                                                                                                                          Caulobacter crescentus
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62.0%;
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                                                     Caulobacter
                                                                         AF027168
AF027168.1
                                                                                                            Caulobacter
                                                                                                                                                 Caulobacter.
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513; Conserv
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Best Local
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ORIGIN
                                                   DEFINITION
                                                                                                                          ORGANISM
                RESULT 29
AF027168
                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                         AUTHORS
                                                                           ACCESSION
                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                    GCTCTGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGAT
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                                                                                                                                                        Length 10667;
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                                                                                                                                                        Score 303; DB 1;
Pred. No. 1.1e-78;
2; Mismatches 302
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                                                                                                                                                        20.3%;
illarity 61.8%;
Conservative
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Best Local S
Matches 496
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Steinman, H.M., Fareed, F. and Weinstein, L.
Direct Submission
Submitted (26-SEP-1997) Biochemistry, Albert Einstein College
Medicine, 1300 Morris Park Avenue, Bronx, NY 10461-1602, USA
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Catalase-peroxidase of Caulobacter crescentus: function stationary phase survival
J. Bacteriol. 179 (21), 6831-6836 (1997)
98012985
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                                      crescentus catalase-peroxidase
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Pred. No. 1.4e-78;
0; Mismatches 308;
    DNA
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1404. .>2885
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    2885 bp
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ILGELERGGLIDASQPTVHAPTMGRALARWIGGRTNSQIAHEFRAAFGGKPTQVAFS
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ALDLVDAMVVAADDSYSDEEVEAIEKAACPTGGSCSGMFTANSMNCLTFALGLSLPGN
GSVLATHADREALFKEAGRVVVDLCQRWYEQEDATALPRGIATRAAFENAMSLDIAMG
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GDASLVGVEPEGGAIEAQGFGWASKHGTGKGPDAITGGPEVIWTQTPTRWSNHFFDNL
FKYEWELTGSPAGAKOWQAKNAPADIPDAFDPNKTHVPRMLTSDLALRFDPAYEKISR
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                        Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                           protein family HMM
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                                                                                                                                       /organism="Caulobacter crescentus CB15"
/strain="CB15"
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Direct Submission
Submitted (31-37M-2001) The Institute for Ge
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
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/gene="CC3044"
                                                                                                                                                                                                /db_xref="taxon:190650"
                                                                                                                                                                                                                                                                                                                                           /note="identified by
TIGR00198"
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/gene="CC3046"
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/gene="CC3045"
                                                                                                                                                                                                                                                            CC3043"
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Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Bleen, J., Heldelberg, J.E., Alley, W.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Blaft, D.H., Kolonay, J.F., Smit, J.J., Craven, M.B., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE005967 10677 bp DNA linear BCT 12-JUN-2002 Caulobacter crescentus CB15 section 293 of 359 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                          1199
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                                                                                                                                                                                                                                                                                                                        1200 ATTTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCGGCTTCCGCGAAAGAT 1259
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      CGCTTCGCCCCCCTGAACAGCTGGCCGGACAACACCAATCTCGACAAGGCCCGCCGCCTG 1838
                                                                                                                                                                              1023 ACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGA 1082
                                                                                                                                                                                                            Caulobacter crescentus CB15
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                               CTGTGGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTG
                                                                                                      GAAGATGACTGGGAGTCGGACCTGGTATACTGGGGGCCTGACAACAAGCCTCTTGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                          AACCGGGATAAAAACG - - - GGAAACTTCAGAAACCTCTTGCCGCCACGCAGATGGGACTT
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Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1440 GGAAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTC 1486
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Submitted (11-MAR-1998) J. Gagnon, Inst. de Biologie Structurale,
41 Avenue des martyrs, F- 38027 Grenobles, FRANCE
Location/Qualifiers
1. 2487
/organism="Haloarcula marismortui"
/db_xref="taxon:2238"
                                                                                                                                                                       963 CTGTGGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTG
                                                                                                                                                                                                                                             1143 AACCGGGATAAAAACG---GGAAACTTCAGAAACCTCTTGCCGCCACGCAGGATGGGACTT
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                                                                                                                                                                                                                                                                                                   GAAGATGACTGGGAGTCGGACCTGGTATACTGGGGGCCTGACAACAAGCCTCTTGCAGAT
                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 2487)
Cannac-Caffrey,V., Hudry-Clergeon,G., Petillot,Y., Gagnon,J.,
Zaccai,G. and Franzetti,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The protein sequence of an archaeal catalase-peroxidase Biochimie 80 (12), 1003-1011 (1998)
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LISDADRKAFEELSATITOHLKTLKLUNNNRIEDLYEOLYAINKRLIGLEGRLLRLADSY
DISNGEFLKAYFGELSATITOHLKTLKLUNNNRIEDLYEOLYAINKRLIGLEGRLLRLADSY
PIDDYRRYTOGYVOKERBRARQAKREWYBANLALVISIAKKYTUNGCLOPLDLYGENIG
LMKAYDKFEYRRGYKESTYATWWIRAITARIADJATIRIPVHMIETINKIVRTSRQ
MILHIGREFPPEELAEKLAMPLEKYRKYLKIAKEPISLETPTGDEBDSHLGDPIEDKN
AILPIDAALOSMLRETTRYLASLIPREERVLRMRFGIGMNTDHTLEEVGGOFSVTRR
RIRQIEAKALRKLKHPSRSRKLRSFLDS
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/product="sensor histidine kinase, putative"
/protein_id="AAKZ5010_1"
/db_xref=101:13424692:
/translation="MSDLERLOPILATALDAVVVMDVEGVVVDWTSRAEVLLGWRREE
VLGRRLSALILDSEAGEGGAEDAALFSSSGRPSLFDVRELMARRQDGGSIAIELSMV
RWSEPDAAPLVLGFVRDISRRSEALKRLVVSEARFRAAIDAVGGVLWTNNASGKWYGE
                                                                                                                           /translation="manlilsvvgsDrpGLTealakavLsAgGNWLESHLSQLGGLYV
GSVLVALDAGSVDALRAAVAEVDAQGLEVRIAPALEAAPAAGETVAFSLVGQDRPGIV
AQVTAVLSGLHANIETFETRLSVEPYSGAPLFHLDARLRLPVTLSASAVQTALEAISG
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Delmkyldperseybaledflamlsbagnnyvaebedaenaedgevarrdenytas
Dkparydpppyrmyllamgsyellsregetalakrieagkdyntsea
Imvmreelgygrillegytblegytaalngyvaaqpaaeddegpaepyddeagkarg
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WRDCLIRAVPLIGDNGEIREWVGVHTDISEQRAAAEKIRESEALFRTLADAAPAPVWM
TEPCGGWEFANAAFAELANVDREALLGYGWLSLLHPDDIAGLLERRQAARAGPDPYTF
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VKNTLASIQSIARQTLRADEVSPRARDQFIDRLMAMSAAHNVLTNERWSGAVIDDILR
EALRPFCDDRDPERITITGPSVRVEPGAALALALAHELGTNAAKYGALSTPHGRVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HWW.
                                                                                                                                                                                                                                                                              protein family HMM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 10677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein family
                                                                                                                                                                                                                                                                                                                                  /product="RNA polymerase sigma factor RpoD"
/protein_id="AAK25009.1"
/db_xref="GI:13424691"
                                                                   /product="conserved hypothetical protein"
/protein_id="AAK25008.1"
/db_xref="GI:13424690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
               'note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.9e-78;
0; Mismatches 308;
                                                                                                                                                                                                                                                                          'note-"identified by match to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="CC3048"
/note="identified by match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 302.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8818. .10587)
/gene="CC3048"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(8818. .10587)
                                                                                                                                                                                                complement(6466. .8424)
/gene="CC3047"
                                                                                                                                                                                                                                         complement(6466. .8424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLPVRVVRADPNDQGPEQVVSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3601 g
                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                     /gene="CC3047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
'gene="CC3046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.3%;
62.0%;
                                                                                                                                                                                 EIMVDVTVGGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3631 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 Similarity 62.0
513; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         663
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ORIGIN
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/translation-"MPEQHPPITETTTGAASNGCPVVGHMKYPVBGGGNQDWMPNRLN
LRVLHQNPPAYADPMGAAEVATTTDVAALTRDIEEVMTSGDPWMPADYGHYGPLF
LRVAMHAAGTYRIHGRGAGGGMQRFAPLNSWPDNRSLDKRRRLLMPVKKKKKKKK
WADLIYFAGNCALESBWGFYFGFGFGRVDQWBPDEVYWGKRATWLGDERYSGKRDLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLAAVQMGLIYVNPEGPNGNPDPMAAAVDIREFFRRMAMNDVETAALIVGGHTFGKTH
GAGPADLVGPEPEAAPLEQMGLGWKSSYGTGTGKDAITSGIEVVWTNTPTKWDNSFLE
ILYGYEWELTKSPAGAWQYTAKDGAGAGTIPDPFGGPGRSPTMLATDLSLRVDPIYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITRRWLEHPEELADEFAKAWYKLIHRHMGPVARYLGPLVPKQTLLWQDPVPAVSHDLV
GEAEIASLKSQIRASGLIVSQLVSTAWAAASSFRGSDKRGGANGGRIRLOPQVGWEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPDGDLRKVIRTLEEIQESFNSAAPGNIKVSFADLVVLGGCAAIEKAAKAAGHNITVP
FTPGRTDASQEQTDVESFAVLEPKADGFRNYLGKGNPLPAEYMLLDKANLLTLSAPEM
TVLVGGLRVLGANYKRLPLGVFTEASESLTNDFFVNLLDMGITWEPSPADDGTYQGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSGKVKWTGSRVDLVFGSNSELRALVEVYGADDAQPKFVQDFVAAWDKVMNLDRFDVR
                                                               1404 GAGCAGGGACTGGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACC 1463
                                                                                           BCT 11-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutation Associated to Isoniazid Resistance in Italian Isolates of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orefici, G.
                                                                                                                                                                                                                                                                                              2223 bp DNA linear BCT 11-FEB-20 gene, complete cds.
AF314111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-OCT-2000) Dip. Biologia Molecolare, Laboratorio di
Microbiologia Molecolare e Biotecnologia, Universita' di Siena,
Viale Bracci, Siena 53100, Italy
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetalas; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 2223)
Orru,G., Iona,E., Memmi,G., Oggioni,M.R., Fattorini,L., and Pozzi,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
9
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    .2223
/organism="Mycobacterium tuberculosis"
/isolate="F27"

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/note="isoniazid resistant isolate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.0%; Score 298.4; DB 1; 62.4%; Pred. No. 1.8e-77; ive 0; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/trans1_table=11
/product="catalase-peroxidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAK06513.]
/db_xref="G1:12744162"
                                                                                                                                                                                  1076 AGCGGTATCGAAGGGCCGTGGAC 1098
                                                                                                                                                        1464 AGTGGCCTGGAAGGAGCCTGGTC 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
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1. 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="katG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="KatG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 2223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o 969
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Best Local Similarity 62.4
Matches 502; Conservative
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                     926
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                                                                                 DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                             /translation-"maetpnsdmsgatggrskrpksnodwwpskinieildonardvg
pveddfdyaeefqxidleavksdleeimtssqdwwpadyghygplfirmawhsagtyr
tadgrggaaggrorfapinswpdnanidkarriilpirqkyggkiswadimilagnva
                                                                                                                                                                                                                                                                                                              KGPGGAWQWAPKSEELKNSVPDAHDPDEKQTPWALITDIALKRDPDYREVMETEQENP
MEKGMNFAKAWYKLTHRDMGPPERFLGPEVPDEEMIWQDPLPDADYDLIGDEEIAELK
EEILDSDLSVSQLVKTAWASASIYRDSDKRGGANGARLRLEPQKNWEVNEPEQLETVL
                                                                                                                                                                                                                                                                                                                                                                                GTLENIQTEFNDSRSDGTQVSLADLIVLGGNAAVEQAAANAGYDVEIPFEPGRVDAGP
EHTDAPSFDALKPKVDGVRNYIQDDITRPAEEVLVDNADLLNLTASELTALIGGMRSI
GANYQDTDLGVFTDEPETLTNDFFVNLLDMGTEWEPAADSEHRYKGLDRDTGEVKWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATG 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGGCATACATTTGGTAAAGCA 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1344 CATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAG 1403
                                                                                                                                                                                                                                               IESMČFKTFGYAGGREDAFEEDKAVNWGPEDEFETQERFDEPGEIQEGLGASVMGLIY
VNPEGPDGNPDPEASAKNIRQTFDRMAMNDKETAALIAGGHTFGKVHGADDPEENLGP
                                                                                                                                                                                                                                                                                         EPEAAPIEQQGLGWQNKNGNSKGGEMITSGIEGPWTQSPTEWDMGYINNLLDYEWEPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990 TCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 CAAAAGATCTCCTGGGCCGACCTGATGATTCTCGCAGGGAACGTCGCCATCGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTCGGACCTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810 CATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGCCGGGGGGCGCCCAGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690 CCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TRIDLIFGSNDRLRAISEVYGSADAEKKLVHDFVDTWSKVMKLDRFDLE"
748 c 795 g 377 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 2487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 300.6; DB 1;
Pred. No. 4.1e-78;
0; Mismatches 294;
                                                                                    /product="peroxidase/catalase"
                                                                                                       /protein_id="CAA76423.1"
/db_xref="G1:2980655"
/db_xref="SPTREMBL:059651"
                                                                 /transl_table=11
                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.2%;
Best Local Similarity 62.6%;
Matches 503; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
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/transl_table=11
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DPDGDLRKVIRTLEELQESFNSAAFGNIKVSFADLVVLGGCAAIERAAKAAGHNITVP
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TYPGGLRVLGANY KR.PLGVFTFASESLTNDFFVNLLDMGTTWESPADDGTYQGRD
GSGKVKWTGSRVGLVFGSNSELRALVEVYGADDAQPKFVQDFVAAWDKVMNLDRFDVR
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ITRRWLEHPEELADEFAKAWYKLIHRDMGPVARYLGPLVPKQTLLWQDPVPAVSHDLV
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   Mutation Associated to Isoniazid Resistance in Italian Isolates Mycobacterium tuberculosis
                                                                            Direct Submission
Submitted (18-OCT-2000) Dip. Biologia Molecolare, Laboratorio di
Submitted (18-OCT-2000) Dip. Biologia Molecolare, Laboratorio di
Microbiologia Molecolare e Biotecnologia, Universita' di Siena,
Viale Bracci, Siena 53100, Italy
Location/Qualifiers
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/organism="Mycobacterium tuberculosis"
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/ba.xref="taxon:1773"
/note="isoniazid resistant isolate"
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Pred. No. 1.8e-77;
); Mismatches 296;
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llarity 62.4%;
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Mycobacterium tuberculosis isolate F16 catalase-peroxidase (katG)
                                                                TGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATG
                                                                                   CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACG
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                                                                                                                                ACCCGATGGGTGCGGCGTTCGACTATGCCGGGAGGTCGCGAACCATCGACGTTGACGCCC 226
                                                                                                                                                                               GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT 867
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                          TATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATA---AAAACGGGAAAC 1164
                                                                                   1284
                                                                                                                                                                                                  CCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGCATACATTTGGTAAAGCAC 1344
                                                                                                                                                                                                                                                          ATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAGG 1404
                                                                                                                                                                                                                                                                                                                   AGCAGGGACTGGGATGGAAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCA 1464
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

I (bases I to 2223)
Orru, G., Iona, E., Memmi, G., Oggioni, M.R., Fattorini, L., Orefici, G. and Pozzi, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutation Associated to Isoniazid Resistance in Italian Isolates of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-ocr-2000) Dip. Biologia Molecolare, Laboratorio di
Microbiologia Molecolare e Biotecnologia, Universita' di Siena,
Viale Bracci, Siena 53100, Italy
                                                                                                     TCTATTGGGGCAAGGAAGCCACCTGGCTCGGCGATGAGCGTTACAGCGGGTAAAGCGGGATC
                                                                                                                                           GTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG
                                                                                                                                                           Argacacca---accasaccararasarasaccasasacrasarasasacrasasac
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protein_id="ARMO519.1"
/db_xref="GI:12744174"
/translation-"MPEQHPPITETTTGAASNGCPVVGHMK'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis isolate F15 truncated catalase-peroxidase (katG) gene, complete cds.
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/isolate="F15"
/db_xref="taxon:1773"
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                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/gene="katG"
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1469 AGCAGGGACTGGGATGGAAAAATAAATGTGGTACAGGAAAGGGCAAATATACCATCACCA 1464
                                                                                                                                                                                                                     1165 ITCAGAAACCTCTIGCCGCCACGCAGGATGGGACTTATTTATGTCAATCCTGAAGGCCCCG 1224
                                                                                                                                                                                                                                                                                              1225 GTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                             1345 ATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCTGCACCTGTGGAGG 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF314121 2223 bp DNA linear BCT 11-FEB-2001
Mycobacterium tuberculosis isolate Rm09 catalase-peroxidase (katG)
 GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         827 ATGGCGCCC---GCCCGGCCGATCTGGTCGGCCCCGAACCCGAGGCTGCTCCGCTGGAGC 883
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Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
I (bases 1 to 2223)
Orru,G., Iona,E., Memmi,G., Oggioni,M.R., Fattorini,L., Orefici,G. and Pozzi,G.
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Submitted (18-OCT-2000) Dip. Biologia Molecolare, Laboratorio di
Microbiologia Molecolare e Biotecnologia, Universita' di Slena,
Viale Bracci, Siena 53100, Italy
Location/Qualifiers
                                                                                                                                                                                                                                            467 GCAAGAAGCTCTCATGGGCGGACCTGATTGTTTTCGCCGGCAACTGCGCGCTGGAATCGA
                                                                                             TCTATIGGGCAAGGAAGCCACCIGGCICGGCGAIGAGCGITACAGCGGTAAGCGGGAIC
                                                                                                                                                                                                                                                                                                                   TGGGATTTAAAAACGCTGGGATTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACCTGG
                                                                                                                                               TATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATA---AAAACGGGAAAC

    1. .2223
    /organism="Mycobacterium tuberculosis"

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/db_xref="taxon:1773"
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/transl_table=11
/product="catalase-peroxidase"
/protein_id="aAR06522.1"
/db_xref="GI:L374180"
/translation="MPEQHPPITETTTGAASNGCPVVGHMKYPVEGGGNQDWMPNRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WADLIVFAGNCALESMGFKTFGFGFGRVDQWEPDEVYWGKEATWLGDERYSGKRDLEN
PLAAVQMGLIYVNPEGPNGNPDPMAAAVDIRETFRRMAMNDVETAALIVGGHTFGKTH
GAGPADLVGPEPEAAPLEQMGLGWKSSYGTGTGKDAITSGIEVVWTNTPTKWDNSFLE
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ITRRWLEHPEELADEFAKAWYKLIHRDMGPVARYLGPLVPKQTLLWQDPVPAVSHDLV
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DPDGDLRKVIRTLEETQESFNSAAPGNIKVSFADLVVLGGGAAIEKAARAAGHNITVP
FTPGRTDASQEQTDVESFAVLEPKADGFRNYLGRGNPLPAEYMLLDKANLLTLSAPEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVLVGGLRVIGANY KRLPLGVFTEASESLTNDFFVNLLDMGITWEPSPADDGTYQGKD
GSGKVKWTGSRVDLVVGSNSELRALVEVYGADDAQPKFVQDFVAAWDKVWNLDRFDVR
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IRWAWHAAGTYRIHDGRGGAGGGMQRFAPLNSWPDNASLDKARRLLWPVKKYGKKLS
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                                                                                           Orefici, G.
                                                                                                                                                                                                                                    Submitted (18-ocr-2000) Dip. Biologia Molecolare, Laboratorio di
Microbiologia Molecolare e Biotecnologia, Universita' di Siena,
Viale Bracci, Siena 53100, Italy
Location/Qualifiers
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                                                                                         Orru, G., Iona, E., Memmi, G., Oggioni, M.R., Fattorini, L.,
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                    Indels

    .2223
/organism="Mycobacterium tuberculosis"
/isolate="An05"

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/note="isoniazid resistant isolate"
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Pred. No. 1.8e-77,
0; Mismatches 296
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/note="KatG"
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llarity 62.4%;
Conservative
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Orru, G.
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                                                                                                          and Pozzi, G.
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Matches 502
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MIU4U593 2223 bp DNA linear BCT 07-JAN-1996 Mycobacterium tuberculosis INH-resistant strain 15726/89, mutant catalase-peroxidase (katG) gene, complete cds.
  AGCAGGGACTGGGAAAAAAAAAATGTGGTACAGGAAACGGCAAATATACCATCACCA 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPEQHPPITETTTGAASNCCPVVCHMKYPVEGGGNODWWPNRLN
LKVLHQNPAVADPMGAAFDYAAEVATIDVDALFRDIEEVMTTSQPWWPADYGHYGPLF
IRMAWHAAGTYRIHDGRGGAGGGMQRFAPLNSWPDNASLDKARRLLWPVKKYGKKLS
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TAAVOWGLITVUNEGPRGNAANDIRETERRAAMNDETALIVGGHFFGKTH
GAGPADLVGFBEPEAPLEQMGLGWKSSYGTGTGKDAITSGIEVWHRIPTKWNDSFLE
ILYGYEWELTKSPAGAWQYTAKDGAGAGTIPDPFGGPGRSPTMLATDLSLRVDPIYER
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GEAETASLKSQIRASGLIVSQLVSTAWAAASSFRGSDKRGGANGGRIRLQPQVGWEVN
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FTPGRTDASQEQTDVESFAVPEPRADGFRNYLGRGNPLPAETMLLDKANLLTLSAPEM
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                         884 AGATGGGCTTGGGCTGGAAGAGCTCGTATGGCACCGGAACCGGTAAGGACGCGGATCACCA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marttila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K.
Direct Submission
Direct Submission
Direct (13-007-1995) Harri J. Marttila, Mycobacterial Reference
Laboratory, National Public Health Institute, Kiinamyllynkatu 13,
Turku, SF-20520, Finland
Location/Qualifiers
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Marttila,H.J., Solli,H., Huovinen,P. and Viljanen,M.K.
katG gene mutations in Isoniazid-resistant Mycobacterium
tuberculosis isolated from Finnish patients
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/strain-"15726/89"
/db_xref-"taxon:1773"
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Pred. No. 1.8e-77;
0; Mismatches 296;
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/protein_id="AAA85167.1"
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                                                                                                         /db_xref="GI:1150696"
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1. .2223
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Best Local Similarity 62.4%;
Matches 502; Conservative
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WADLIVFAGNCALESMGFKTFGFGFGRVDQWEPDEVYWGKEATWLGDERYSGKRDLEN
PLAAVQMGLIYVNPEGPNGNPDPMAAAVDIRETFRRAMMNDVETAALIVGGHTFGKTH
                                                                                                                                                                            GAGPADI.VGPEPEAAPI.EQMGLGWKSSYGTGTGKDA.ITSGIEVWWTNFPTKWDNSFILE
ILVGYEWELTKSPAGANQYTAKDGAGAGTIEDPFGGFGRSPTWLATDIS.EKNUDFIYER
ILTERWI.EHPEELADERAKWYKI.HRDMGPVARXLGFLVPRQTLIMODPVPAVSHDLV
GEAEIASLKSQIRASGIIVSQLVSTAMAAASSFRGSDRRGGANGGRIRLQPQYGWEVN
                                                                                                                                                                                                                                                            DPDGDLRKVIRTLEELQESFNSAAPGNIKVSFADLYVLGGCAAIEKAAKAAGHNITVP
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                                                                                               LKVLHQNPAVADPMGAAFDYAAEVATIDVDALTRDIEEVMTTSQPWWPADYGHYGPLF
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Pred. No. 1.8e-77;
0; Mismatches 296;
            /product="catalase-peroxidase"
/protein_id="AAK06523.1"
/db_xref="GI:12744182"
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/protein_id-"AAA85169.1"
/db_xref-"G1.50700"
/translation-"MPEQHPPITETTTGAASNGCPVVGHMKYPVEGGGNQDWWPNRLN
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IRMAWHAAGTYRIHDGRGGAGGGMQRFAPLNSWPDNASLDKARRLLWPVKKKYGKKLS
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PLAAVQMGLIYVNPEGPNGNPDPMAAAVDIRETFRRWAMNDVETAALIVGGHTFGKTH
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ILVGYEWELTKSPAGANQYTAKDGAGAGTIPDPEGGGRSPYMLATDISLRVDPIYER
IITRWIJEHPEELADERAWYKLIHEDMGPVRYLGPLYPROTILLWODPVPAYSHDLY
GEAEIASLKSOIRASGLIVSQLVSTAWAAASSFRGSDKRGGANGGRIRLQPQVGWEVN
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FTPGRTDASORDTVESFAVLERKADGERNILGKORPLLAESTKLLDKRALLTLEAPEM
FTVLVGGLRVLGANYRRLPLGYFTEASESLTNDFYNILDMGTTWEPSPADDGTYQGKD
GSGKVKWTGSRVDLVFGSNSELRALVEVYGADDAQPKFVQDFVAAMDKVMNLDDREDVR
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 2 (bases 1 to 2223)
Martila, H.J., Solil.H., Huovinen,P. and Viljanen,M.K.
Direct Submission
Submitted (13-NOV-1995) Harri J. Marttila, Mycobacterial Reference
Laboratory, National Public Health Institute, Kiinamyllynkatu 13,
Turku, SF-20520, Finlans
Location/Qualifiers
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Pred. No. 1.8e-77;
0; Mismatches 296;
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/db_xref="taxon:1773"
/note="INH-resistant strain"
                                                                                                                                                     /organism="Mycobacterium
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/transl_table=11
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Mycobacterium tuberculosis INH-resistant strain H0251/90, mutant
                                                          GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT
                                                                                                                                 928 CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGGGCCAGTCAAGAAAAATACG
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                                   TGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATG
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                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria, Actinobacteridae, Actinomycetales; Corynebacterineae; Mycobacterium; Mycobacterium; Mycobacterium; Mycobacterium; Mycobacterium; Lo 2223)
Martila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K. KatG gene mutations in Isoniazid-resistant Mycobacterium tuberculosis-strains isolated from Finnish patients
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U40595.1 GI:1150699
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Mycobacterium tuberculosis
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Mycobacterium tuberculosis strain=H0055/92
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                                               Score 298.4; DB Pred. No. 1.8e-77
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THMWHAAGTYRIHOGRGGAGGGMQREAPLASWPDNASLDKARRLLMPVKKYGKKLS
WADLIVFACNCALESMGFKTFGFGFGRVDQWBPDEVYWGKEATWLGDERYSGKRDLEN
PLAAVQMGIITVNNFGFGPNGNPDPMAAAVDIRETFRRWAMNDVETAALIVGGHTFGKTH
GAGPADLVGPEPEAAPLE"
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protein_id="aAA85111.1"
/db_xref="GI:LI5704"
/translation="MPEQHPPITETTIGAASNGCPVVGHMKYPVEGGGNQDWMPNRLN
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Submitted (27-NOV-1995) Harri J. Marttilla, Mycobacterial Reference
Laboratory, National Public Health Institute, Kiinamyllaynkatu 13,
Turku, SF-20520, Finland
Location/Qualiflers
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                                                             706
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                                              TCTATTGGGGCAAGGAAGCCACCTGGCTCGGCGATGAGCGTTACAGCGGGTAAGCGGGATC
                                TICAGAAACCICITGCCGCCACGCAGAIGGGACTIAITIAIGICAAICCIGAAGGCCCCG
                                                                                                                CCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGCATACATTTGGTAAAGCAC
                                                                                                                                                                                     GTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG
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Martilla H.J., Solni, H., Huovinen, P. and Viljanen, M.K.
katG gene mutations in Isoniazid-resistant Mycobacterium
tuberculosis strains isolated from Finnish patients
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Direct Submission
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Mycobacterium tuberculosis
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/db_xref="taxon:1773"
/note="INH-resistant strain"

    .2223
    /organism="Mycobacterium"

                                                                                                                                                                                                                                                                                                                                                            GTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                                                                                                                                                                                                                                                                                                             /note="mutant katg"
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/gene∞"katG"
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MTU41305
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TITLE
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BCT 07-JAN-1996
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Marttila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K.
Marttila, G.J., Soini, H., Huovinen, P. and Viljanen, M.K.
Direct Submission
Submission
Submission
Submission
Submission
Submission
Laboratory, National Public Health Institute, Kiinamyllaynkatu 13,
Turku, SF-20520, Finland
Location/Qualifiers
    GCAAGAAGCTCTCATGGGCGGACCTGATTGTTTTCGCCGGCAACTGCGCGGAATCGA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis INH-resistant strain H0004/93, mutant catalase-peroxidase (katG) gene, complete cds.
                                                                                                                                                                                                                                                                                                                       1225 GTGGAAAACCAGATCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 884 AGATGGGCTTGGGCTGGAAGAGCTCGTATGGCACCGGAACCGGTAAGGACGCATCACC
                                               1048 TGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACCTGG
                                                                         1108 TATACTGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATA---AAAACGGGAAAC
                                                                                                                                                                                                                                                              1285 CCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGGCGTACATTTGGTAAAGCAC
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1 (bases 1 to 2223)
Marttila, H.J., Solii, H., Huovinen, P. and Viljanen, M.K. katG gene mutations in Isoniazid-resistant Mycobacterium tuberculosis strains isolated from Finnish patients
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/organism="Mycobacterium tuberculosis"
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/db_xref="taxon:1773"
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FLAAVOMGLITYVNEGPRORDPDMAAAVDIRETRRAAMNUSTBALLYGGHFGKTH
GAGPADLIVGPEPEADLEDNGLGWKSSYGTGTGKDA.TISGIEVWHTRTPTKWDNSFLE
ILYGYEWELTKSPAGAWOYTAKDGAGAGTIPDPFGGPGRSPTMLATDLSLRVDPIYER
ITRRALLENPEBEADERAKAWYKLIHRDMGPVARYCHDLVDPOYDVANDIYER
GEBELASLKSQIRAGGITVOSQIVYSTAWAAASFRCSDKRGGANGGRIRLOPOYDAVGHEVD
DPDGDLRKVIRTLEELQESFNSAAPGNIKVSFADLVVLGGCAAIEKAAKAAGHNITVP
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LKVLHQNPAVADPMGAAFDYAAEVATIDVDALTRDIEEVMTTSQPWWPADYGHYGPLF
IRMAWHAAGTYRIHDGRGAGGGMQRFAPLNSWPDNASLDKARRLLWPVKKYGKKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVLVGGLRVLGANYKRLPLGVFTEASESLTNDFFVNLLDMGITWEPSPADDGTYQGKD
GSGKVKWTGSRVDLVFGSNSELRALVEVYGADDAQPKFVQDFVAAWDKVMNLDRFDVR
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                                                                                                                                                                                                     2 (bases 1 to 2223)
Martila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K.
Direct Submission
Submitted (27-NOV-1995) Harri J. Marttila, Mycobacterial Reference
Laboratory, National Public Health Institute, Kiinamyllaynkatu 13,
Turku, SF-20520, Finland
Location/Qualifiers
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                                                             Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 2223)
Marttila,H.J.; Solni,H.; Huovinen,P. and Viljanen,M.K. katG gene mutations in Isoniazid-resistant Mycobacterium tuberculosis strains isolated from Finnish patients
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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/organism="Mycobacterium tuberculosis"
/strain="#0055/92"
/db_xref="taxon:1773"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="catalase-peroxidase"
/protein_id="AAA85172.1"
/db_xref="GI:1150706"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="INH-resistant strain"
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MTU41313 2223 bp DNA linear BCT 07-JAN-1996 Mycobacterium tuberculosis INH-resistant strain H0211/94, catalase-peroxidase (katG) gene, complete cds.
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LKVLHQNPAVADPMGAAFDYAAEVATIDVDALTRDIEEVMTTSQPWWPADYGHYGPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLAAVQMGLIYVNPEGPNGNPDPMAAAVDĪRETFRRMAMNDVETAALIVGGHTEGKTH
GAGPADLVGPEPEAAPLEQMGLGWKSSYGTGTGKDAIISGIEVVWTNTPTKWDNSFLE
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ITRRWLEHPEELADEFAKAWYKLIHRDMGPVARYLGPLVPKQTLLMQDPVPAVSHDLV
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FTPGRTDASQEQTDVESFAVLEPKADGFRNYLGKGNPLPAEYMLLDKANLLTLSAPEM
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GSGKVKWTGSRVDLVFGSNSELRALVEVYGADDAQPKFVQDFVAAWDKVMNLDRFDVR
    884 AGATGGGCTTGGGCTGGAAGAGCTCGTATGGCACCGGAACCGGTAAGGACGCGATCACCA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 2223)
Marttila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K.
Direct Submission
Submitted (27-NOV-1995) Harri J. Marttila, Mycobacterial Reference
Laboratory, National Public Health Institute, Kiinamyllaynkatu 13,
Turku, SF-20520, Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ACCCGATGGGTGCGCGCTTCGACTATGCCGCGGGGGGGCCCGACCGTCGACGTTGACGCCC 226
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 2223)
Marttila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K.
KatG gene mutations in Isoniazid-resistant Mycobacterium
tuberculosis strains isolated from Finnish patients
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    .2223
/organism="Mycobacterium tuberculosis"
/strain="H0211/94"

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/protein_id="AAA85179.1"
/db_xref="GI:1150720"
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Pred. No. 1.8e-77
); Mismatches 29
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                                              1465 GTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                    /db_xref-"taxon:1773"
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/gene="katG"
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                                 /translation="MEDGNEPTTETTGAASNGCPVVGHMKYPVBGGGNQDWWPNRLN
LKVLHQNPAYADPWGAAFDYAAEVATIDVDALTRDIEEVWTTSQPWWPADJGHYGPLF
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IRWAHAAGTYR THORGGAGGMORRAPLNSWPDNASLDRARRLAPPYKKYGKKLS
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ITRRHLEHPEELADEFAAWYKLIHEDMGPYARTGGFLVPRQTLLWQDPVPRYSHDLV
GEAETASLKSGIRASGLTVSQLVSTAWAAASSFRGSDKRGGANGGRIRLQPQVGWEVN
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TVLVGGLRVLGANYKRLPLEARAGSSTRTNDFFNNLLDMGTYWERDFYRGKD
GSGRVKWTGSRVDLVFGPNSELRALVEVYGADDAGFKYQDFVAAWDKVMNLDRFDVR
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Pred. No. 1.8e-77;
0; Mismatches 296; Indels 6;
/protein_id="AAA85176.1"
/db_xref="G1:1150714"
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LKVLHQNPAVADPMGAAFDYAAEVATIDVDALTRDIEEVMTTSQPWWPADYGHYGPLF
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  Laboratory, National Public Health Institute, Kiinamyllaynkatu 13,
Turku, SF-20520, Finland
Location/Qualifiers
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Pred. No. 1.8e-77;
0; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                   /transl_table=11
/product=catalase-peroxidase"
/protein_id="AAAA8180.1"
/db_xref="G1:1150722"
                                                                                                                                                                    /note="INH-resistant strain"
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    . 2223
    /organism="Mycobacterium
/strain="H0725/93"
    /db_xref="taxon:1773"

                                                                                                                                                                                                                                         1. .2223
/gene="katG"
/note="mutant katG"
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Marttila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K.
Direct Submission
Submitted (27-NOV-1995) Harri J. Marttila, Mycobacterial Reference
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                                                                                                                                                                                                                                                                  826
TGACGCGGGACATCGAGGAAGTGATGACCACCTCGCAGCCGTGGTGGCCCGCCGACTACG
                                                                                                                                                                      CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACG
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                                                                     ATGATGCCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGC
                                               GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT
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Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterinum tuberculosis complex.
1 (bases 1 to 2223)
Marttila, H.J., Soini, H., Huovinen, P. and Viljanen, M.K. katG gene mutations in Isoniazid-resistant Mycobacterium tuberculosis strains isolated from Finnish patients
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FTPGRTDASQEQTDVESFAVLEPKADGFRNYLGKGNPLPAEYMLLDKANLHLRSVPLR
                                                                           Score 298.4; DB 1;
Pred. No. 1.8e-77;
0; Mismatches 296;
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DPDGDLRKVIRTLEEIQESFNSAAPGNIKVSFADLVVLGGCAAIEKAAKAAGHNITVP
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                                 1225 GTGGAAAACCAGATCCTCTGGCTTCCGGGAAAGATATCAGGGGAAGCTTTTTCACGTATGG 1284
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                                                                                                                                                                                                                                            707 ACGCAACCCGGACCCCATGGCCGCGGGGGTCGACATTCGCGACGTTTCGGCGCATGG 766
 TGGAGAACCCGCTGGCGGGTGCAGATGGGGCTGATCTACGTGAACCCGGAGGGGCCGA 706
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Mycobacterium tuberculosis INH-resistant strain H0078/91, mutant
catalase-peroxidase (katG) gene, complete cds.
                                                                                                               827 ATGGCGCCG---GCCCGGCCGATCTGGTCGGCCCCGAACCCGAGGCTGCTCCGCTGGAGC
                                                                                                CCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGGCATACATTTGGTAAAGCAC
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/product="catalase-peroxidase"
/protein_id="AAA85170.1"
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/note="mutant katG"
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Cockerill,F.R., Kline,B.C. and Uhl,J.R.
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Patent: US 568639-A 1 18-NOV-1997;
Location/Qualifiers
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Pred. No. 1.8e-77;
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                                                             M. tuberculosis
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                                                                                                                                                                Length 2235;
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                                Cockerill, F.R. III, Kline, B.C. and Uhl, J.R. Detection of isoniazid resistant strains of Patent: US 5658733-A 1 19-AUG-1997; Location/Qualifiers
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Pred. No. 1.8e-77, 0; Mismatches 29
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Cockerill,F.R., Uhl,J.R., Temesgen,Z., Zhang,Y., Stockman,L.,
Roberts,G.D., Williams,D.L. and Kiline,B.C.
Rapid identification of a point mutation of the Mycobacterium
tuberculosis catalase-peroxidase (katG) gene associated with
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Mycobacterium; Mycobacterium tuberculosis complex.
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FGKTHFGFGRAWQTARAGGGAGTIPDFFGGFGRSFTMLAFDLSLRVDFYRE
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ITRRWILEHPEELADEFAKAWYKLIHRDMGPVARYLGPLVPKQTLLWQDPVPAVSHDLV
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FTPGRTDASQEQTDVFSFAVLEPKADGFRNYLGKGNPLPAEYMLLDKANLLTLSAPEM
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AGCAGGGACTGGGATGGAAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCA 1464
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Mycobacterium tuberculosis L33308 catalase (katg) gene, complete
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                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
                        Cockerill, F.R., Uhl, J.R., Temesgen, Z., Zhang, Y., Stockman, L., Roberts, G.D., Williams, D.L. and Kline, B.C.
Rapid Identification of a point mutation of the Mycobacterium tuberculosis catalase-peroxidase (katG) gene associated with
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Pred. No. 1.8e-77;
0; Mismatches 296; Indels 6;
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                                                                                             876 ATGCCCCCG---GCCCGGCCGATCTGGTCGGCCCCGAACCCGAGGCTGCTCCGCTGGAGC 932
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                   GTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG
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Cockerill, F.R., Uhl, J.R., Temesgen, Z., Zhang, Y., Stockman, L., Roberts, G.D., Williams, D.L. and Kline, B.C.
Rapid Identification of a point mutation of the Mycobacterium tuberculosis catalase-peroxidase (katG) gene associated with isoniazid resistance
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Submitted (07-FEB-1994) Bruce C. Kline, Mayo Clinic and Mayo
Foundation, Biochemistry and Molecular Biology, 200 SW 1 St.,
Rochester, MN 55905, USA
Location/Qualifiers
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69. .2291
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Kline, B.C.
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MADLIYPGARAWLGDBRYSGKRKYDGWEBDEVWGKREAWHGDBRSYGKRDLEN
PLAAVQMGIIYNDEDENGGRPDPMAAVDIRETFRWAMNDVETAALVGGFFFGKTH
GAGPADLVGPEPEAAPLEOMGLGWKSSYGTGTGKDAITSGIEVVWTNTPTKWNNSFLE
ILYGYBWEBLYKSPAGAMQYTAKDGAGAGTIPDPGGPGRSPYMLATDLSLRVDPIYER
ILYGYBWEBLABPERLABAWTKLIHRDMGYARYLGFLYPKQTLLWODPVPRYSHDLY
GEAEIASLKSOIRASGLIVSGLVSTAWAAASSFRGSDKRGGAWGGRIRLQPOVGWEVN
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FTGFRUDSOSQOTVVESFAVLEPKADGFRNILGKROPLPAEPTHLLDKRALLTLESPEM
TVLVGGLRVLGANY KRLP KGVFTEASESLTNDFFVNILLDMGTTWEPSPADDGTY OGKO
GSGKVKWTGSRVDLVFGSNSELRALVEVYGADDAQPKFVQDFVAAWDKVMNLDRFDVR
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                                            Kline, B.C.
Direct Submission
Submitted (07-FEB-1994) Bruce C. Kline, Mayo Clinic and Mayo
Foundation, Blochemistry and Molecular Biology, 200 SW 1 St.,
Rochester, MN 55905, USA
On Jul 23, 1996 this sequence version replaced g1:488431.
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    . 2311
    /organism="Mycobacterium tuberculosis"

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Pred. No. 1.8e-77;
0; Mismatches 296;
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/db_xref="GI:1439531"
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ITRRWLEHPEELADEFAKAWYKLIHRDMGPVARYLGXLVPKQTLLMQDPVPAYSHDLV
GEBELASKAKSQIRASGLIYOQLYSTAMAAASSFRGSDKRGGANGGRIRLQPQVGWEVN
DPDGDLKKVIRTLEELGESFREDGSFRAPONIKVSFADLVVLGGCAAIEKAAKAAGHNITVP
FTPGRTDASOEQTDVESFAVLEPKADGFRNYLGKGNPLPAEYMLLDKANLLTLSAPEM
TYLVGGLRVLGANYKRLPLGYFTEASESLTNDFFVNLLDMGITWEPSPADDGTYQGKD
          PLAAVQMGLIYVNPEGPNGNPDPMAAAVDIRETFRRMAMNDVETAALIVGGHTFGKTH
GAGPADLVGPEPEAAPLEQMGLGWKSSYGTGTGKDAITSGIEVVWTNTPTKWDNSFLE
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Pred. No. 1.8e-77;
0; Mismatches 296; Indels '6;
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GAGPADLVQRGPEPAAPLEQMGLGWKSSYGTGTGKAAITSGIEVWTHNFPKWDNSFLE
ILYGYEWELTRSPAGAMQYTRADGAGAGTIPDPFGGERSPTHLATDLSLRVDPIYER
ITRRWLEHPEELADEFAKAWYKLIHRDMGPVARYLGPLVVPKQTLLMQDPVPAVSHDLY
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GSGKVKWTGSRVDLVFGSNSELRALVEVYGADDAQPKFVQDFVAAWDKVWNLDRFDVR
                                  MTU06260 2326 bp DNA linear BCT 20-MAY-1994
Mycobacterium tuberculosis G6108 catalase (katG) gene, complete
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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Rapid identification of a point mutation of the Mycobacterium tuberculosis catalase-peroxidase (katG) gene associated with isoniazid resistance
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submission Submitted (07-FEB-1994) Bruce C. Kline, Mayo Clinic and Mayo Foundation, Blochemistry and Molecular Biology, 200 SW 1 St., Rochester, MN 55905, USA Location/Qualifiers
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    .2326
/organism="Mycobacterium tuberculosis"
/strain="G6108"

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Cockerill, F.R., Uhl, J.R., Temesgen, Z.,
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Search completed: June 18, 2003, 04:52:44 Job time: 2697.55 secs

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Sequence 1415, A Sequence 1411, Ap Sequence 1411, Ap Sequence 152, App Sequence 352, App Sequence 463,
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Scoring table:

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Minimum DB Maximum DB

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US-09-764-847-1415
US-09-1764-847-1414
US-09-18-154-1414
US-09-912-154-1414
US-09-912-2598-352
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US-09-912-2598-352
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US-09-991-403-352
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| Cgn2_6/ptodata/1/pubpna/DSO7_pUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_bUBC_DBS.seq:*
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| Cgn2_6/ptodata/1/pubpna/USO8_bUBCOMB.seq:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-10-184-644-332
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Pred. No. 6.4e-110;
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           FILE REFERENCE: DIVERIIOO-4
CURRENT APPLICATION NUMBER: US/09/884,889
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 09/412,347
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1997-10-16
PRIOR FILING DATE: 1997-0-10-16
PRIOR FILING DATE: 1996-07-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                            ; TYPE: DNA
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1337 TAAAGCACATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACC 1396

828 1397 888

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TGTGGAGGAGCAGGACTGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATAC 1456

947

Sequence 7, Application US/09884889 Patent No. US20020102680A1 GENERAL INFORMATION: APPLICANT: DIVERSA CORPORATION
APPLICANT: ROBERTSON, Dan
APPLICANT: SANTAL, Indrajit
APPLICANT: ADHIKARI, Robert
TITLE OF INVENTION: CATALASES US-09-884-889-7

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1261 TCAGGGAAGCTTTTTCACGTATGGCCATGGATGAGGAGACTGTGGCCCTGATCGCGG 1320
                                                                                                                                                                                                                                 1321 GAGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAG 1380
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         994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSWPRILPTGIRAEQVNKKGIEFYSDLIDALLSSNITPIVTLHHWDLPQLLQVKYGGWQN 171
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                                                                                                                                              935 ACCCAAAAGCCTCTGACGTTGAAAACCAGGGCTTAGGTTGGGGCAACCCCAACATGCAGG
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R103
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
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Best Local Similarity 9.2%; Pred. No. 0.047;
Matches 41; Conservative 134; Mismatches 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 254, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION:
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Stewart, Timothy A
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742 AGGCTCTGAAAAAAATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGG 801
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Pred. No. 9.2e-65;
0; Mismatches 329; Indels
APPLICANT: BUYERSA CORPORATION
APPLICANT: ROBERTSON, Dan
APPLICANT: ROBERTSON, Dan
APPLICANT: ROBERTSON, Dan
APPLICANT: ADHIKARI, ROBERT
TITLE OF INVENTION: CATALASES
FILE REFERENCE: DIVERIL100-6-19
CURRENT APPLICATION NUMBER: US/09/884,889
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 09/412,347
PRIOR APPLICATION NUMBER: US 08/51,844
PRIOR FILING DATE: 1997-10-16
PRIOR FILING DATE: 1997-10-16
PRIOR FILING DATE: 1996-07-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Alcaligenes (Deleya) aquamarinus US-09-884-889-5
                                                                                                                                                                                                                              Sequence 5, Application US/09884889 Patent No. US20020102680A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.1%;
Best Local Similarity 57.4%;
Matches 476; Conservative
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Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Wood, William I.
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Zyskind, Judith W.
                                                                                                                                            Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 20.2%
Matches 53; Conservative
                                                                                                                                                                                           Pan, James
Smith, Victoria
                                                                                                                                                                                                                                                            Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-332
                                             Sequence 332, Application No.
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APPLICANT:
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APPLICANT:
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                                                                                                                                                           1190 GAIGGGACTIATITAIGICAAICCIGAAGGCCCCGGIGGAAAACCAGAICCICIGGCTIC 1249
                                                                                              1130 GCCTCTTGCAGATAACCGGGATAAAAACGGGGAAACTTCAGAAACCTCTTGCCGCCACGCA 1189
                                                              292 NPIYAGDYPQVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITE 351
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   HIIKAHAKTWHSYNTTWRSKQQGLVGISLNCDWGEPVDISNPKDLEAAERYLQFCLGWFA 291
                                                                                                                           352 RNYPSRQGPSYQNDRDLIELVDPNWPDLGSKWLYSVPWGFRRLLNFAQTQYGDPPIYVME 411
                                                                                                                                                                                        412 NGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIKGYTSWSLLDKFEWEKGYSDRY 471
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MGRDGATGPSGPQGPPGVKGEAGLQGPQGPQGPKGSKGDGGLIGPKGE 242
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CURRENT APPLICATION NUMBER: US/206-28
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
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20.2%; Pred. No. 1;
Live 58; Mismatches 152; Indels
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Publication No. US20030044930A1
GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William I.
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Best Local Similarity 20.2%
Matches 53; Conservative
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US-10-184-644-332
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1223 CGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTAT 1282
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CURRENT APPLICATION NUMBER: 2002-06-28
FILE REPERT FILING DATE: 2002-06-28
FILE NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 MGRDGATGPSGPQGPPGVKGEAGLOGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGE
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58; Mismatches 152; Indels
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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20.2%; Pred. No. 1;
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Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.
Application US/10184634
5. US20030068684A1
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Gaps

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655 ATAATITITITAATTTATCTGGTTCTTCAGTAGCACTTGTCACGATTGAAAAACTATACG 596
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                                                                                                                                                                                                                       Length 927;
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FILE REFERENCE: ELTTRA.011A
FILE REFERENCE: ELTTRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                 Query Match 2.3%; Score 34.2; Di
Best Local Similarity 49.7%; Pred. No. 2.1;
Matches 87; Conservative 0; Mismatches
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Best Local Similarity 49.7%; Pred. No. 2.5;
Matches 87; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4832, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Staphylococcus aureus US-09-815-242-4832
                            TYPE: DNA ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ohlsen, Kari L.
Zyskind, Judith W.
Wali, Daniel
Trawick, John D.
Carr, Grant J.
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                                                                                                                                  ; LOCATION: (1)...(927)
US-09-815-242-8989
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                                                                                                        NAME/KEY: CDS
LENGTH: 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 AAAGTICAAAIGCIICIGCAICIIGGAAAIIGCCIIIITIAICACGCAACICAICIAAIA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603 GCCGCTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAA 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                    PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 2188
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/205,578
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8989, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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                            ION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-2188
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APPLICANT: Syskind, Judith W.
PPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
FILING DATE: 2000-03-21
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543 AAAAAACTCTTCCTGTTCTGATTCTTCTGGCGCTATCGGGGAGCTTTTCTACCGCTGTA 602
                                961 ATAATTTTTTAATTTATCTGGTTCTTCAGTAGCACTTGTCACGATTGAAAAACTATACG 902
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                                                                                                                                                                                                                               APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 ATAATTTTTTAATTTATCTGGTTCTTCAGTAGCACTTGTCACGATTGAAAAACTATACG 524
                                                              603 GCCGCTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAA 657
                                                                                         Gaps
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486,33
OPERATING STERM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                              E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                   US-08-781-986A-565

Sequence 565, Application US/08781986A

Publication No. US20030054436A1

GRERAL INFORMATION:

APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-8504
TELEPRAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 565:
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: double
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Matches 87; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                              Rockville
                                                                                                                                                                                                                                                                                                                                                                Maryland
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STATE: Ma
COUNTRY:
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US-09-764-891-8918/C Sequence 8918, Application US/09764891 ; Publication No. US20030077808A1 ; GENERAL INFORMATION:

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 ICTGAGATTACACAGCCCTGAATCAAATCCCTGGGGGCTGATTTTGATTATGCCACCAG 721
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
ENG ID NO 8918
LENGTH: 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 9; Length 636;
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0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICATION NUMBER: PCI/US01/00666
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00667
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: US 60/207,456
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APPLICATION NUMBER: US 09/632,366
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PAPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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Patent No. US20020048763A1
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Best Local Similarity 59.2%;
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8918
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801 GATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATAC
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Best Local Similarity 6.6%; Pred. No. 1.8;
Matches 32; Conservative 156; Mismatches 298;
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Smith, Victoria
Watanabe, Colin K
Wood, William I.
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Gurney, Austin L.
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Goddard, Audrey
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US-10-184-634-592
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APPLICANT: Godowski, Paul J.
APPLICANT: Bun, James
APPLICANT: Bun, James
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND CLERE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: 93430R10227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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                                                                                                                                                                                                                             CTHER INFORMATION: MAP TO AL035457.11

CTHER INFORMATION: EXPRESSED IN HERRT, SIGNAL = 0.85

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.094

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.93

US-09-864-761-3110
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Conservative 156; Mismatches 298; Indels
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 592
LEMOTH: 499
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine Vers. 1.1
SEQ ID NO 3110
LENGTH: 457
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5. US20030044930A1
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1 Similarity 56.9%;
62; Conservative
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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US-10-184-644-592
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Matches 32; Conserva
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Best Local S
Matches 62
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129 DDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEPVEANSEES
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430NTCE: P340NTCE: P3430NTCE: P3430NTCE: P3430NTCE: P3430NTCE: P3430NTCE: P340NTCE: P3430NTCE: 
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Best Local S
Matches 59
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                                  861 AGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAAC 920
                                                                                                        921 AGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAA 980
                                                                                                                                                                                                     309 EYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEEDKVQLTVP 368
129 DDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEPVEANSEES 188
                                                                                                                                   249 NSSQVSNEQDKIDAYKLLKKEWTLDLKTKRGSTADALVSDDETTRLVTSLEDDFDEELDT 308
                                                                                                                                                                                                                                                                                369 PGIKNDDKNILTTWGDTIFSIVTGGEETRDTWDLESSSSEEEREDDDDALVPDSKQGKPQ 428
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                                                            189 DSVFSENTEDLOEQFTTOKHHSHANSOANHAQGEQASFESFEEMLQDKLKVPESENNKTS
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C12
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Best Local Similarity 57.8%; Pred. No. 2;
Matches 59; Conservative 0; Mismatches 43;
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CURRENT FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 340
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Patent No. US20020165371A1
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; LCCATION: 383, 453, 465, 501
; OTHER INFORMATION: n = A,T,C or G
US-09-924-400-147
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Harlocker, Susan L.
Day, Craig H.
Li, Samuel X.
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Dillon, Davin C.
Retter, Marc W.
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                                                                                                                                                                                                                                          APPLICANT: HATLOCKEY, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121, 419C11
CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
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2.3%; Score 33.8;
al Similarity 57.8%; Pred. No. 2;
59; Conservative 0; Mismatche
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SOFTWARE: FastSEQ for Windows Version 3.0
LENGIH: 579
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Sequence 147, Application US/09810936
Patent No. US20020068285A1
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Patent No. US20020111467A1
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; OTHER INFORMATION: n = A,T,C or G
US-09-810-936-147
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; OTHER INFORMATION: n - A,T,C or
US-09-429-755-147
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Skeiky, Yasir A.W
                                                               APPLICANT: Frudakis, Tony N. APPLICANT: Reed, Steven G. APPLICANT: Smith, John M.
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Dillon, Davin C.
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Reed, Steven G.
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Retter, Marc W.
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ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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426 ILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLLSLAFHPNYKKNGKLYVSY 485
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT APPLICATION NUMBER: US/10/184,634
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 012
                                                                     499 TACAACAIGCGAATTICCCTTAAICCGGAGCTATICGTAIGATAAAAAAAACTCTICCTG
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                                          439 CTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAAGTTGACTTTTGTA
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2.3%; Score 33.8; Di
Best Local Similarity 8.1%; Pred. No. 2.7;
Matches 46; Conservative 161; Mismatches
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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APPLICANT: Chen, Jian
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US-10-184-634-574
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddowski, Paul J.
APPLICANT: Goddowski, Paul J.
APPLICANT: Goddowski, Paul J.
APPLICANT: Gorney, Austin L.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: Shood, William I.
APPLICANT: Shood, William I.
APPLICANT: Shood, William I.
APPLICANT: APPLICANT: ACTOR ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: U5/10/184,644
CURRENT FILING DATE: 2002-06-28
FILOR PROPERTING PATE: 2002-06-28
MUMBER: OF SEQ ID NOS: 612
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                                                                                                                               246 GGEMICGGFYPRISCCIRSDSPGLGRIENKIFSVTNNTECGKLLEEIKCALCSPHSQSLF 305
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                    Length 579;
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46; Conservative 161; Mismatches 361; Indels
                                                              Indels
                                                                                                                                                                                         1376 CGCAGGGCCTGATGGTGCACCTGTGGAGGAGCAGGGACTGGG 1417
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                    DB 10;
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                 Score 33.8; DB Pred. No. 2; 0; Mismatches
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Publication No. US20030044930A1
               2.3%;
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                                                            59; Conservative
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US-10-184-644-574
                                      Similarity
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Best Local Similarity
Matches 46; Conserva
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RESULT 22
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439 CTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAAGTTGACTTTTGTA 498
                                                                                                                                                                                                                                             499 TACAACAIGCGAATITCCCTTAAICCGGAGCTAITCGTAIGAIAAAAAAAAACTCTTCCIG 558
                                                                                                                                                                                                                                                                                                            546 FLYIILGDGMITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNSTNQPPE 605
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                                                                                                                                                                   86 TINQERWALGPHDHILRVVEYIVSTRNPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDG
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US-10-092-154-1415/c

Sequence 1415, Application US/10092154

Publication No. US20030054375A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: US/10/092,154

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2003

PRIOR APPLICATION FORCES

SOFTWARE: PARENTE TO FROM TO SECONS

SOFTWARE: PARENTE IN VENTION FROM TO SECONS

SOFTWARE: PARENTE IN VENTION OF TO SECONS

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SOFTWARE PARENTE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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Patent No. US20020132767A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003

SOFTMARE: patentIN Ver. 2.0
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Pred. No. 16;
0; Mismatches 51;
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Pred. No. 16;
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Best Local Similarity 55.7%;
Matches 64; Conservative
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Best Local Similarity 55.7%;
Matches 64; Conservative
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CORGANISM: HOMO SapienS
US-10-092-154-1415
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US-09-764-847-1415
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LENGTH: 6383
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LENGTH: 6383
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1303 CTGTGGCCCTGATCGCGGGAGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTG 1362

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15674 CIGCAGGTGTACGCGGTGGAGGCCACTGAGATGCCACAGGCACACGGGGCAGCTGGTCCTG 15615
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Sequence 1414, Application US/09764847

Sequence 1414, Application US/09764847

GENERAL INCORMATION:

TITLE OF INFORMATION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC009

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT FILIA DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 2003

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                    RESULT 21
US-10-022-154-1414/C
Sequence 1414, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION:
TILLE OF INVENTION:
TILLE REPREBLE:
CURRENT APPLICATION NUCLEIC ACIDS, Proteins, and Antibodies
FILLE REPREBLE: 2009C1
CURRENT APPLICATION UNGHER: US/10/092,154
CURRENT APPLICATION UNGHER: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
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SEQ ID NO 1414
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Pred. No. 37;
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Best Local Similarity 55.7%;
Matches 64; Conservative
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Best Local Similarity 55.7%;
Matches 64; Conservative (
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-918-995-29551
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LENGTH: 21732
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R APPLICATION NUMBER: 60/08861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08875
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                   R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/083322
R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
                                                                                                       R FILING DATE: 1997-11-13

R APPLICATION NUMBER: 60/066770

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/075945

R FILING DATE: 1998-02-25

R APPLICATION NUMBER: 60/078910
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R PAPLICATION NUMBER: 60/088212

R PILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088217

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088655

R FILING DATE: 1998-06-09
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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PILING DATE: 1998-06-10

FILING DATE: 1998-06-10

APPLICATION NUMBER: 60/088858

FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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ILING DATE: 1998-06-04
PPLICATION NUMBER: 60/088026
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PPLICATION NUMBER: 60/088029
ILING DATE: 1998-06-04
PPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
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PPLICATION NUMBER: 60/088326
LING DATE: 1998-06-04
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ILING DATE: 1998-06-10
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PELICATION NUMBER: 60/088028
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PPLICATION NUMBER: 60/088202
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                                                                                 APPLICATION NUMBER: 60/065311
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FILING DATE: 1998-06-03
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FILING DATE: 1998-06-04
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                                               GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 29551
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2.2%; Score 33.2; Di
Best Local Similarity 57.8%; Pred. No. 2.9;
Matches 59; Conservative 0; Mismatches
Sequence 29551, Application US/09918995
Publication No. US20030073623A1
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| LCCATION: (1)...(484)
| CTHER INFORMATION: n = A,T,C or G
US-09-918-995-29551
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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US-09-992-598-352
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089948
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PPLICATION NUMBER: 60/090355
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ILING DATE: 1998-06-24
PPLICATION NUMBER: 60/090445
PPLICATION NUMBER: 60/089514
ILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090252
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ING DATE: 1998-06-24
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PLICATION NUMBER: 60/090435
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APPLICATION WINBER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090695
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TLING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090863
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FILING DATE: 1998-06-26
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
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Best Local Similarity 54.0%; Pred. No. 11;
Matches 6%; Conservative 0; Mismatches
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                                                      PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
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FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                      APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Botstein, David
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US-09-989-293A-352
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R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
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R APPLICATION NUMBER: 60/090557
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FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 LING DATE: 1998-Ub-12
PLICATION NUMBER: 60/090246 PPLICATION NUMBER: 60/090431 LLING DATE: 1998-06-24 PPLICATION NUMBER: 60/090435 LLING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 LING DATE: 1998-06-25
PLICATION NUMBER: 60/090696
LING DATE: 1998-06-25 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 LING DATE: 1998-06-17 PLICATION NUMBER: 60/089538 :LING DATE: 1998-06-17 PLICATION NUMBER: 60/089599 LING DATE: 1998-06-17 LING DATE: 1998-06-16
PPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 FILING DATE: 1998-Ub-22
APPLICATION NUMBER: 60/090254
TTT NOT ATTE: 1998-06-22 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/090444 LICATION NUMBER: 60/089514 LICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/089801 PLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/090695 1998-06-25 998-06-17 1998-06-17 1998-06--90-866 LING DATE:

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R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/066770
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/075945
R FILING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
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R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
R APPLICATION NUMBER: 60/087609
R APPLICATION NUMBER: 60/087599
R APPLICATION NUMBER: 60/087759
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R APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088655
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3226;
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Best Local Similarity 54.0%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches
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CURRENT FILING DATE: 2001-11-19
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PRIOR PLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
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PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-07
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                                         DR APPLICATION NUMBER: 60/091360
DR FILLING DATE: 1998-07-01
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DR APPLICATION NUMBER: 60/091544
DR FILLING DATE: 1998-07-01
DR APPLICATION NUMBER: 60/091519
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DR FILLING DATE: 1998-07-02
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Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: ASTMENAZI, AVI J.
60/090863
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PRIOR APPLICATION NUMBER: 60/049787
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Gurney, Austin L.
Kljavin, Ivar J.
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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
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Paoni, Nicholas F
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Botstein, David
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2118 ATGAGC 2123
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PRIOR APPLICATION NUMBER: 60/08538
PRIOR APPLICATION NUMBER: 60/08538
PRIOR PRILING DATE: 1989-66-17
PRIOR APPLICATION NUMBER: 60/08560
PRIOR APPLICATION NUMBER: 60/08560
PRIOR APPLICATION NUMBER: 60/08560
PRIOR PRINCE DATE: 1989-61-18
PRIOR PRILING DATE: 1989-61-18
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PRIOR PRINCATION NUMBER: 60/090659
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1415 GGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGGGGCCTGGA 1474
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091549
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091682
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Eaton, Dan L.
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Best Local Similarity 54.0%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches
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                                                                R APPLICATION NUMBER: 60/090863
R FILING DATE: 1998-66-26
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R APPLICATION NUMBER: 60/091360
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
Ferrara, Napoleone
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Gerber, Hanspeter
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Pan, James
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APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090695
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1355 GICICCIGAAAAAIGIATIGGCGCAGGGCCIGAIGGIGCACCIGIGGAGGAGGAGGACI 1414 1998 GTCTCATTAACAATGCATTCAGCTCGTCAGCATTGGGAAGCTGTCCATTGAAAAGGCCT 2057 1415 GGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGA 1474 Gaps TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITTLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PIC14 58; Indels DB 9; Query Match 2.2%; Score 33.2; Di Best Local Similarity 54.0%; Pred. No. 11; Matches 68; Conservative 0; Mismatches PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091636
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PRIOR PILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07 Sequence 352, Application US/09990436 Publication No. US20020198148A1 GENERAL INFORMATION: ILING DATE: 1998-06-26
PPLICATION NUMBER: 60/090863
ILING DATE: 1998-06-26 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 Grimaldi, J.Christopher Gurney, Austin L. Watanabe, Colin K. Williams; P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Ferrara, Napoleone Fong, Sherman Gerritsen, Mary E. Goddard, Audrey Paoni, Nicholas F. Gerber, Hanspeter APPLICANT: Ashkenazi, Avi J. Baker, Kevin P. Botstein, David Kljavin, Ivar J Desnoyers, Luc Napier, Mary A. Godowski, Paul 1475 AGGAGC 1480 1118 ATGAGC 2123 09-990-436-352 APPLICANT APPLICANT g ò ŏ 셤

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CURRENT FILING DATE: 3010-11-15

PRIOR APPLICATION NUMBER: 60/06226

PRIOR PELING DATE: 1997-10-17

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Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/090696
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PRIOR FILING DATE: 1998-07-09
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
Desnoyers, Luc
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Pan, James
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
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1998-06-23
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FILING DATE: 1998-06-24
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ö 1415 GGGATGGAAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGA 1474 1355 GTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAGGAGCAGGGACT ö Indels Pred. No. 11; 0; Mismatches Score 33.2; Pred. No. 11 PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-07-01
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PRIOR PILING DATE: 1998-07-07 Sequence 352, Application US/09993687 Publication No. US20020198149A1 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 PRIOR APPLICATION NUMBER: 60/091982 PRIOR FILING DATE: 1998-07-07 PRIOR APPLICATION NUMBER: 60/092182 PRIOR FILING DATE: 1998-07-09 Grimaldi, J.Christopher Query Match 2.2%; Best Local Similarity 54.0%; Matches 68; Conservative (Roy, Margaret Ann Stewart, Timothy A. Ferrara, Napoleone Fong, Sherman Gerritsen, Mary E Paoni, Nicholas F. Gerber, Hanspeter Gurney, Austin L. APPLICANT: Ashkenazi, Avi J. Botstein, David Baker, Kevin P. Goddard, Audrey Desnoyers, Luc Napier, Mary A Godowski, Paul Kljavin, Ivar Eaton, Dan L. 1475 AGGAGC 1480 2118 ATGAGC 2123 US-09-993-687-352 APPLICANT ò 엽 ò g à

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Watanabe, Colin K. Williams, P. Mickey Wood, William I.

Daniel

ON: Acids Encoding the Same P2730P1C11 RRENT APPLICATION NUMBER: US/09/993,687 CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13 R APPLICATION NUMBER: 60/083322 R FILING DATE: 1998-04-28 A APPLICATION NUMBER: 60/084600 R FILING DATE: 1998-05-07 A APPLICATION NUMBER: 60/087106 R FILING DATE: 1998-05-28 R FILING DATE: 1998-06-03

R APPLICATION NUMBER: 60/088021

R R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088025

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R APPLICATION NUMBER: 60/088039

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IR FILING DATE: 1998-06-05
IR FILING DATE: 1998-06-09
IR FILING DATE: 1998-06-09
IR APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-05-28
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FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/08824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/08826 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08861 ILING DATE: 1998-06-05 1998-06-04 01-90-866 PRIOR
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FILING DATE: 1998-06-25

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                                                                             CURRENT APPLICATION NUMBER: US/09/989,734 CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-03-25
PRIOR PAPLICATION NUMBER: 60/08450
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FILING DATE: 1998-06-11
                                                  FILE REFERENCE: P2730P1C64
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R APPLICATION NUMBER: 60/090863
R-FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
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                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/091978
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/091544
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Best Local Similarity 54.0%;
Matches 68; Conservative
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Gerber, Hanspeter
Gerritsen, Mary E.
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tewart, Timothy
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Eaton, Dan L.
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APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089801
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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ILING DATE: 1998-06-25
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0; Mismatches
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090862
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PRIOR PELING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091360
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Publication No. US20030004311A1
GENERAL INFORMATION:
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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Best Local Similarity 54.0%;
Matches 68; Conservative
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APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
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ITLE OF INVENTION:
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PRIOR PILING DATE: 1997-12-11
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PRIOR PILING DATE: 1998-01-23
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-19
R PAPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
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Publication No. US20030008297A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
                                       APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/090538
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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Gurney, Austin L.
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Stewart, Timothy A.
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Fong, Sherman
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Goddard, Audrey
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Desnoyers, Luc
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APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10

Watanabe, Colin K. Williams, P. Mickey

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APPLICATION NUMBER: 60/089948
APPLICATION NUMBER: 60/089952
PELING DATE: 1998-06-19
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
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R FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090435
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ING DATE: 1998-06-25
LICATION NUMBER: 60/090678
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
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ILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090690
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/090535
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Sequence 352, Application US/09993667 Publication No. US20030022187A1 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

Desnoyers, Luc

Eaton, Dan L.

Grimaldi,J.Christopher

Godowski, Paul

APPLICANT

Gurney, Austin L. Kljavin, Ivar J.

APPLICANT

Napier, Mary A.

Gerritsen, Mary E. Goddard, Audrey

Gerber, Hanspeter

Roy, Margaret Ann Stewart, Timothy

Tumas, Daniel Watanabe, Colin

APPLICANT: APPLICANT:

Danie

Paoni, Nicholas F

APPLICANT

Ferrara, Napoleone Fong, Sherman

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Best Local Similarity 54.0%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches
                     PRIOR FILING DATE: 1938-00-25
PRIOR FILING DATE: 1938-06-25
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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NG DATE: 1998-06-22
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090429
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                                              IILE OF INVENTION: Secreted and Transmembrane PolyPeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
                                                                                            CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
                                                                                                                                               FILING DATE: 1997-06-16
APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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FILING DATE: 1997-11-12
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ING DATE: 1997-11-13
LICATION NUMBER: 60/066770
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FILING DATE: 1998-02-25
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NG DATE: 1998-03-20
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LLING DATE: 1998-04-28
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1998-05-07
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APPLICATION NUMBER: 60/087827
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LICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088030
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ILING DATE: 1998-06-04
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ILING DATE: 1998-06-04
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PPLICATION NUMBER: 60/088167
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PPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088826
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ILING DATE: 1998-06-10
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Williams, P. Mickey
Wood, William I.
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                                                                                LE REFERENCE: P2730P1C4
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                                   hang, Zemin
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2058 TGGATTTATCCCTGTACTTGAAACATGAAACTGAAATTATGCCCGTGTTTCAAGGTTTGA 2117
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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0; Mismatches
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CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 550
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5. US20030022328A1
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Best Local Similarity 54.0%;
Matches 68; Conservative
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Wood, William
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APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
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                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-463
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2118 ATGAGC 2123
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GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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1 Similarity 54.0%; Pred. No. 11;
68; Conservative 0; Mismatches
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APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION UNDRER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091519
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Wood, William
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Filvaroff, Ellen
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Gurney, Austin L
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US-10-121-049-463
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FITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11-12
PRIOR PLICATION NUMBER: 60/065186
PRIOR PELICATION NUMBER: 60/065186
PRIOR PELICATION NUMBER: 60/065181
PRIOR PELING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/075945
PRIOR PLICATION NUMBER: 60/075945
PRIOR PLICATION NUMBER: 60/075945
PRIOR PRILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088025
                           Grimaldi, J.Christopher
Gurney, Austin I.
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-09
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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FILING DATE: 1998-06-04
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - See Palm or File Wrapper
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                                                                                                                                                                             Sequence 463, Application US/10140470
Publication No. US20030022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Publication No. US20030027754A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Baton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Stewart, Timothy A.
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DeForge, Laura
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Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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Filvaroff, Ellen
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Gurney, Austin L
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Best Local Similarity 54.08
Matches 68; Conservative
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 463
LENGTH: 3226
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1475 AGGAGC 1480
                                     2118 ATGAGC 2123
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; ORGANISM: Homo Sapien
US-10-140-470-463
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R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
R PRING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
R PELLING DATE: 1998-06-23
R FILING DATE: 1998-06-23
R PELLING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090459
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
R FILING DATE: 1998-06-24
R PELLING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/089801
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08824
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/088861
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1415 GGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGA
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Best Local Similarity 54.0%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches
                                                   PRIOR APPLICATION NUMBER: 60/090542
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR APPLICATION NUMBER: 60/090679
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PELING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090695
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R APPLICATION NUMBER: 60/090540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/091982 PRIOR FILING DATE: 1998-07-07 PRIOR APPLICATION NUMBER: 60/092182 PRIOR FILING DATE: 1998-07-09
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
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2118 ATGAGC 2123
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-10
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ILING DATE: 1998-06-17
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FILING DATE: 1998-06-11
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LICATION NUMBER: 60/089514
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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FILING DATE: 1998-06-17
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NG DATE: 1998-06-17
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090254
                                                                                  FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/1
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TNG DATE: 1998-06-1:
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LING DATE: 1998-06-1
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                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PRILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-02-25
PRIOR PRILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/075945
PRIOR PRILING DATE: 1998-02-25
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R APPLICATION NUMBER: 60/086025
R APPLICATION NUMBER: 60/086026
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/086028
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/086029
R FILING DATE: 1998-06-04
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088033
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(LING DATE: 1998-06-05
Grimaldi, J.Christopher
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FILING DATE: 1998-06-05
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Williams, P. Mickey
Wood, William I.
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                                                                                                            yy, Margaret Ann
ewart, Timothy
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                                                                                      Paoni, Nicholas F
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                      Gurney, Austin
                                                      pier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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APPLICATION NUMBER:
                                                                                                                                         umas, Danie
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AFPLICANT: Anany. Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PL44

CURRENT PAPLICATION NUMBER: US/09/997,428

CURRENT PILING DATE: 1201-11-15

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1998-04-25

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PRIOR PILING DATE: 1998-04-28

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R FILING DATE: 1998-06-04
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R FILING DATE: 1998-06-04
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R FILING DATE: 1998-06-04
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RR FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088031
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R APPLICATION NUMBER: 60/087827
R FILING DATE: 1998-06-03
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R APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/087759
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-05
                        Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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                                             Gurney, Austin L.
Kljavin, Ivar J.
                                                                                          Napier, Mary A.
    Godowski, Paul
                                                                                                                Pan,James
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Publication No. US2003002716241
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Fertara, applieone
APPLICANT: Fertara, applieone
APPLICANT: Gerber, Hanspeter
             R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090542

R FILING DATE: 1998-06-24

R PILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090676
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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FILING DATE: 1998-07-01.
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-09
ICATION NUMBER: 60/090540
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088861
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TLING DATE: 1998-06-17
PPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/08824
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/089801
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PPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089908
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PPLICATION NUMBER: 60/090252
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090472
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Best Local Similarity 54.0%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches
              PRIOR APPLICATION NUMBER: 60/090540
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090676
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-09
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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
1998-06-24
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APPLICANT: Baker, Kevin P.
APPLICANT: Betstein, David
APPLICANT: Desnoyers, luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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US-09-997-666-352
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R APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089952
R APPLICATION NUMBER: 60/090246
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R FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089538
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PLICATION NUMBER: 60/089598
LING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/090431
               APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
                                                       PLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/090254
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60-90-8661
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CURRENT APPLICATION NUMBER: 05/09/997,666
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
                                                                                                                                                                                                                                                                                                                                                                                                                          R FILING DATE: 1997-06-16
R APPLICATION NUMBER: 60/062250
R FILING DATE: 1997-10-17
R APPLICATION NUMBER: 60/065186
R FILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065311
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A APPLICATION NUMBER: 60/086029

R FILING DATE: 1998-06-04

A APPLICATION NUMBER: 60/086030

R FILING DATE: 1998-06-04

A APPLICATION NUMBER: 60/086033
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APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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FILING DATE: 1998-03-20
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NPPLICATION NUMBER: 60/087759
TLING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088025
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NPLICATION NUMBER: 60/088326
TLING DATE: 1998-06-04
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FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-05-07
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FILING DATE: 1998-06-03
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                                    Srimaldi,J.Christopher
Gurney,Austin L.
                                                                                                                                                                                                                    Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                        Roy, Margaret Ann
Stewart, Timothy P
Tumas, Daniel
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                                                                                                                                       Paoni, Nicholas F
                                                                             Kljavin, Ivar J
                                                                                                  pier, Mary A.
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                                                                                                                                                                                                                                                                                       Zemin
                                                                                                                      an, James
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1415 GGGATGGAAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGA 1474
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                                                                                                                                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P333041253 CURRENT APPLICATION NUMBER: US/10/175,746 CURRENT FILING DATE: 2002-06-19
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3226;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 463
LENGTH: 3226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
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FILE REFERENCE: P3330R1C382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2%;
                                                                                                                                                       Tumas, Daniel
Watanabe, Colin K
Wood, William
      Godowski, Paul J.
Gurney, Austin L.
                                                                                                                        Stewart, Timothy
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Wood, William
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Best Local Similarity 54.0
Matches 68; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
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                                                                                            Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-175-746-463
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LENGTH: 3226
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54.0%; Pred. No. 11;
.ive 0; Mismatches
PRIOR FILING DATE: 1998-06-24
PRIOR PELIGATION NUMBER: 60/090540
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR PILING DATE: 1998-06-24
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PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090678
PRIOR PILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090690
PRIOR PELING DATE: 1998-06-26
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Publication No. US20030027270A1
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APPLICANT: Beresini, Maureen
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Best Local Similarity 54.0
Matches 68; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
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                                                                 DB 9; Length 3226;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 463
                                                               Query Match 2.2%; Score 33.2; D
Best Local Similarity 54.0%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 463, Application US/10176921
Publication No. US20030027276A1
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresin1, Maureen
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Goddard, Audrey
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
Gao, Wei-Qianq
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Matches 68; Conservative
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ORGANISM: Homo Sapien
US-10-176-921-463
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RESULT 46

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Transmembrane Polypeptides and Nucleic
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R APPLICATION NUMBER: 60/083322

R RELLING DATE: 1998-04-28

R APPLICATION NUMBER: 60/084600

R RILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/087106

R APPLICATION NUMBER: 60/087106

R APPLICATION NUMBER: 60/087607

R APPLICATION NUMBER: 60/087607

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R APPLICATION DATE: 1998-06-02
Application US/09990711
5. US20030032023A1
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APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
AAPPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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                                                                                                          APPLICANT: Ashkenazi, Avi J.
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Botstein, David
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                                                                       SENERAL INFORMATION
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APPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-04
R PILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088202
OR RPILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088212
OR APPLICATION NUMBER: 60/088212 R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17

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R RILING DATE: 1998-06-17 RILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
RILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
RILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60,088824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60,088826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60,088858
FILING DATE: 1998-06-11 R APPLICATION NUMBER: 60/089653 R FILING DATE: 1998-06-17 R APPLICATION NUMBER: 60/089801 R PILING DATE: 1998-06-18 R APPLICATION NUMBER: 60/089907 R FILING DATE: 1998-06-18 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 TLING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
APPLICATE: 1998-06-12 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 PPLICATION NUMBER: 60/090246 ILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 PRIOR

1355 GTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAGGAGGAGGAGTT 1414 1415 GGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGA 1474 Length 3226; DB 9; Query Match
2.2%; Score 33.2; D
Best Local Similarity 54.0%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-24

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PRIOR PRILING DATE: 1998-06-24

PRIOR PELICATION NUMBER: 60/090540

PRIOR PELICATION NUMBER: 60/090676

PRIOR PELICATION NUMBER: 60/090676

PRIOR PELICATION NUMBER: 60/090676

PRIOR PELICATION NUMBER: 60/090690

PRIOR PELICATION NUMBER: 60/09140

PRIOR PELICATION NUMBER: 60/09150

PRIOR PELICATION NUMBER: 60/09163

RIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 1475 AGGAGC 1480 PRIOR PRIOR ö g 셤 à ò

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9330HZ51
CURRENT APPLICATION NUMBER: 105/10/142,431
CURRENT FILING DATE: 2002-05-10
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Pred. No. 11;
0; Mismatches 58; Indels
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SEQ ID NO 463
LENGTH: 3226
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Pred. No. 11;
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Best Local Similarity 54.0%;
Matches 68; Conservative
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Goddard, Audrey
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Beresini, Maureen
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Watanabe, Colin K
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Sherwood, Steven
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Filvaroff, Ellen
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Best Local Similarity 54.0
Matches 68; Conservative
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US-10-142-431-463
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33300R10154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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Pred. No. 11;
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Best Local Similarity 54.0%;
Matches 68; Conservative (
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Stewart, Timothy A
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Wood, William
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DeForge, Laura
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Goddard, Audrey
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
Gao, Wel-Qiang
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C211
CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
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Matches 68; Conservative 0; Mismatches
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Publication No. US20030036180A1
GENERAL INFORMATION:
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
                                                                1475 AGGAGC 1480
                                                                                      TYPE: DNA
CORGANISM: Homo Sapien
US-10-143-114-463
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US-09-328-314-7
US-09-328-314-7
US-09-35-528-31
US-09-42-936-61
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PCT-US94-01149-17
US-09-11-192A-145
US-08-95-316-85
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US-09-249-181A-1

US-08-136-574A-1

US-08-804-227C-7

US-09-804-198-1

US-09-126-316-11

US-09-282-147-38

US-09-342-055-1

US-09-126-316-11

US-09-126-316-31

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US-09-082-614A-45

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          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPBERATING SYSTEM: Windows95
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,887A
FILING DATE: 03-JUL-1996
PRICH APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                     NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09015/002001
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                     TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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NAME: Haile, Ph.D., Lisa
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STRANDEDNESS: double
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Best Local Similarity
Matches 542; Conserv
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US-09-385-742B-8

US-08-213-419B-3

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US-08-213-419B-3

US-08-213-605-5

US-08-915-648-41

US-08-915-848-41

US-08-929-843-41

US-08-929-843-41

US-08-13-488-31

US-08-13-488-31

US-08-21-107-66

US-09-232-201-66

US-09-232-201-66

US-09-232-107-66

US-08-32-107-65

US-08-32-107-66

US-08-32-107-66

US-08-32-267A-13

US-08-32-267A-13

US-08-33-427-1

US-09-323-427-1

US-09-323-427-1

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Patent No. 593300
GENERAL INFORMATION:
APPLICANT: Robertson, Dan E.
APPLICANT: Sanyal, Indrajit
APPLICANT: APPLICANT: APPLICANT:
ITLE OF INVENTION: CATALASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Ri
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AGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTC 1276

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ZIP: 92037 COMPUTER READABLE FORM:

CITY: La STATE: CA

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1337 TAAAGCACATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACC 1396
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                       863 GACATATGATGGCCGGGGGGCGCCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAG
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
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APPLICANT: Robertson, Dan E.
APPLICANT: Sanyal, Indrajit
APPLICANT: Adhikari, Robert S.
TITLE OF INVENTION: CATALASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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; Patent No. 6410290
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66.7%; Pred. No. 6.8e-107;
11ve 0; Mismatches 264;
                                                                                                                                                                                                       1457 CATCACCAGTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                           948 CATCACCAGTGGACTAGAAGCCGCCTGGACCA 979
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APPLICATION NUMBER: US/08/951,844
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/674,887
FILING DATE: July 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019
REFERENE/POCKET NUMBER: 331400-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08951844
Patent No. 6074860
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: RODETSON et al.
TITLE OF INVENTION: Catalases
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
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Matches 542; Conservative
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STATE: NEW JERSI
COUNTRY: USA
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828 AAAAACCCATGGTGCTGCCGATGCGGAGAAATATGTGGGCCGAGAGCCTGCCGCCGCAGG 887
                                                                         888 TATTGAAGAAATGAGCCTGGGGTGGAAAAACACCTACGGCACCGGACACGGTGCGGATAC 947
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                                                                                                                                                                                                                                             Sequence 1, Application US/08418782
Patent No. 5658733
GENERAL INFORMATION:
APPLICANT: Cockerill, Franklin R.
APPLICANT: Kline, Bruce C.
APPLICANT: Kline, Bruce C.
APPLICANT: MIN. Detection of Isoniazid Resistant Strains TITLE OF INVENTION: Detection of Isoniazid Resistant Strains NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 296;
                                                                                                               1457 CATCACCAGTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                                                                     948 CATCACCAGTGGACTAGAAGGCGCCTGGACCA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
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Pred. No. 1.8
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WOESSNET, WATERD D.
REGISTRATION NUMBER: 30,446
REFERENCE, POCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: single
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                                                                                                                                                                                                                         US-08-418-782-1
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Pred. No. 6.8e-107;
0; Mismatches 264; Indels
                                                                                                                         09015/002001
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/674,887
                                                                       NAME: Halle, Ph.D. Lisa A.
REGISTRATION NUMBER: 38,347
REFRENCE/DCCKET UNDBER: 0901:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                  Coding Sequence 1...2235
                                                             ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 66.79
Matches 542; Conservative
                                                                                                                                                                                                                                                                                              linear
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MOLECULE TYPE:
                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-09-412-347-7
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
                                                                                                              DNA (genomic)
                                                          LENGTH: 2235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                 Query Match 20.0
Best Local Similarity 62.4
Matches 502; Conservative
                       TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                  linear
                                                                                                 TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                        US-08-228-662-1
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                                                            GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCA 1047
                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGGGACTGGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCA 1464
                                                                                                                                                            TATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATA---AAAACGGGAAAC 1164
                                                                                                                                                                                                           TICAGAAACCICTIGCCGCCACGCAGAIGGGACTTATITATGTCAATCCTGAAGGCCCCG 1224
                                                                                                                                                                                                                         GTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG
                                                                                                                                                                                                                                                                                     716 ACGGCAACCCGGACCCCATGGCCGCGGCGGTCGACATTCGCGAGACGTTTCGGCGCATGG
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           CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACG
                                                                                  GCAAGAAGCTCTCATGGGCGGACCTGATTGTTTCGCCGGCAACTGCGCGCTGGAATCGA
                                                                                                           TGGGATTTAAAACGCTGGGATTTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACCTGG
                                                                                                                         APPLICANT: COCKERILL, FRANKLIN R.
APPLICANT: KLINE, BRUCE C.
APPLICANT: UHL, JAMES R.
TITLE OF INVENTION: DETECTION OF ISONIAZID RESISTANT STRAINS
TITLE OF INVENTION: OF M. TUBERCULOSIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SCHWEGNAN, LUNDBERG & WOESSNER, P.A. STREET: 3500 IDS CENTER CITY: MINNEAPOLIS STATE: MINNESOTA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WOESSNER, WARKEN D.
RESISTRATION UNMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.123US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGCCTGGAAGGAGCCTGGTCGA 1488
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08228662 Patent No. 5688639 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                            TGAAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATG
                                                                                                                                                                  ATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGC
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                                       Gaps
                                     9
   Length 2235
                                     Indels
   DB 1;
                                   0; Mismatches 296;
                    Pred. No. 1.8e-87
20.0%; Score 298.4; 62.4%; Pred. No. 1.8
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1108 TATACTGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATA---AAAACGGGAAAC 1164
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536 TGGGCTTCAAGACGTTCGGGTTCGGCTTCGGCCGGGTCGACCAGTGGGAGCCCGATGAGG 595
                                                                          596 TCTATTGGGGCAAGGAAGCCACCTGGCTCGGCGATGAGCGTTACAGGGGGTAAGGCGGGATC 655
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APPLICANT: COCKETIL, Bruce C.
APPLICANT: Kline, Bruce C.
APPLICANT: MI, James R.
TITLE OF INVENTION: Detection of Isoniazid Resistant Strains
TITLE OF INVENTION: of M. Tuberculosis
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lundberg & Woessner
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5658733
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 20
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NAME: WOOSSNET, WAITEN D.
REGISTRATION NUMBER: 30,4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Schwegman, In
T: 3500 IDS Center
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2331 base pairs
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ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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                  APPLICANT: Cockerill, Franklin R. APPLICANT: Kline, Bruce C. APPLICANT: Kline, Bruce C. APPLICANT: Uhl, James R. TITLE OF INVENTION: Detection of Isoniazid Resistant Strains TITLE OF INVENTION: of M. Tuberculosis NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSE: Muchi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2235;
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                                                                                                                                                                                                                         ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 5922575th Fourth Street, Ste. 203
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 298.4; DB 2;
Pred. No. 1.8e-87;
0; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230.00010130
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,219
FILING DATE: 07-May-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          Sequence 1, Application US/08852219
Patent No. 5922575
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sandberg, Victoria A.
REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2235 base pairs
                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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Best Local Similarity 62.4%
Matches 502; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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1108 TATACTGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATA---AAAACGGGAAAC 1164
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    Detection of Isoniazid Resistant Strains of M. Tuberculosis
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                                                                                                                                                 COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,219
FILING DATE: 07-May-1997
CLASSIFICATION: 435
ATTONREY/AGERT INFORMATION:
NAME: Sandberg, Victoria A:
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 230.00010130
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 612-305-1226
                                              CORRESPONDENCE ADDRESS:
ADDRESSEE Mucting, Raasch & Gebhardt, P.A.
STREET: 119 No. 5922575th Fourth Street, Ste. 203
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 20.0%; Score 298.4; DB 2; Best Local Similarity 62.4%; Pred. No. 1.9e-87; Matches 502; Conservative 0; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: EDUGHH: 2331 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 70..2289
   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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US-08-852-219-20
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                                                                                                                                         748 TGAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATG
                                                                                                                                                                                                   928 CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACG
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                                                                                                                                                                                                                                                                                                         868 ATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGC
                                                                                              Gaps
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9
                                                            Length 2331;
                                                            20.0%; Score 298.4; DB 1; Length 62.4%; Pred. No. 1.9e-87; ive 0; Mismatches 296; Indels
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Patent No. 5922575
GENERAL INFORMATION:
APPLICANT: Cockerill, Franklin R. APPLICANT: Kline, Bruce C.
APPLICANT: Uhl, James R.
                                                                                            Conservative
 CDS
70..2289
                                                                            al Similarity 502; Conserv
; NAME/KEY:
; LOCATION:
US-08-418-782-20
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2152723 TGGAGAACCGCTGGCCGCGGTGCAGATGGGGCTGATCTACGTGAACCCGGAGGGCCGA 2152664
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2152903 GCAAGAAGCICICAIGGGGGGACCIGAITHIII I H H II II IIIIII I
                                                 GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCA
                                                                                                                                            2152843 TGGGCTTCAACACGTTCGGCTTCGGCTTCGGCCGGTCGACCAGGGGGGCCCGATGAGG
                                                                                                                    TGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACCTGG
                                                                                                                                                                                        TATACTGGGGGCCTGACAACCTCTTGCAGATAACCGGGATA---AAAACGGGAAAC
                                                                                                                                                                                                                                                             TTCAGAAACCTCTTGCCGCCACGCAGATGGGACTTATTATGTCAATCCTGAAGGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: FIRISCHMAN, Robert D.
APPLICANT: WITTE, Owen R.
APPLICANT: WITTE, Owen R.
APPLICANT: WITTE, Owen R.
APPLICANT: WITTE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICANTION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 4411529;
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Pred. No. 1.8e-85;
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; ORGANISM: Mycobacterium tuberculosis
; CTER INFORMATION: H37Rv
US-09-103-840A-1
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Best Local Similarity 62.4%;
Matches 502; Conservative
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LENGTH: 4411529
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US-09-103-840A-1/c
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                                                                                                                                                                                                                                                                                                           TTCAGAAACCICTTGCCGCCACGCAGATGGGACTTATTTATGTCAATCCTGAAGGCCCCG 1224
                                                                                                                                                                                                                                                                                 AGCAGGGACTGGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCA 1464
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                         1225 GTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG
                                                                                                   776 ACGCAACCCGGACCCCATGGCGCGGGGGTCGACATTCGCGAGACGTTTCGGCGCTGG
                                                                                                                                                                                                              ATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAGG
                                                                                                                                                             GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCRMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: WITE, OLD C.
TITLE OF INVENTION: TUBERCILOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113203 ACCCGATGGGTGCGGCGTTCGACTATGCCGCGGAGGTCGCGCCACCATCGACGTTGACGCCC
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Pred. No. 1.8e-85;
0; Mismatches 296; Indels 6; G
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                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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Best Local Similarity 62.4%;
Matches 502; Conservative
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SEQ ID NO 2
LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Length 2221;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,782
                                                                                                                                                                                                                                                                                                                                                                           Score 274.2; DB 1;
Pred. No. 1.6e-79;
0; Mismatches 303;
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WGGSENEY, WARTEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
                                                                                                                         30,440
                                                                                                                                                                                              TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           18.4%;
Similarity 61.4%;
                                                                                                                                                                                                                                                 LENGTH: 2221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA
US-08-418-782-2
                                                                                                                                                                                                                                                                                                          linear
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Best Local Simi
Matches 493;
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                                                     2155643 GCAAGAAGCTCTCATGGGGGGGACCTGATTGTTTTCGCCGGCAACTGCGCGCTGGAATCGA 2155584
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                                   GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT
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Patent No. 5658733
GENERAL INFORMATION:
APPLICANT: Cockerill, Franklin R.
APPLICANT: Kline, Bruce C.
APPLICANT: Mll, James R.
ITILE OF INVENTION: Detection of Isoniazid Resistant Strains
TITLE OF INVENTION: of M. Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lundberg & Woessner
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman.
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STATE: MN
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988 GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAA--TGTTGCCCTTGAATC 1045
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             834 TGGCGCCG---GCCCGGCCGATCTGGTCGGCCCCGAACCCGAGGCTGCTCCGCTGGAGCA 890
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                                                                                                                                             1046 CATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACCT
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APPLICANT: Kline, Bruce C.
APPLICANT: Uhl, James R.
TITLE OF INVENTION: Detection of Isoniazid Resistant
TITLE OF INVENTION: of M. Tuberculosis
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 5922575th Fourth Street, Ste. 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5922575
GENERAL INFORMATION:
APPLICANT: Cockerill, Franklin R.
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NAME: Sandberg, Victoria A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 23
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1406 GCAGGGACTGGGATGGAAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCAG 1465
                   688 ATCCCTGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTC 747
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APPLICANT: COCKERILL, FRANKLIN R.
APPLICANT: KLINE, BRUCE C.
APPLICANT: WILL, TAMES R.
TITLE OF INVENTION: DETECTION OF ISONIAZID RESISTANT STRAINS
TITLE OF INVENTION: OF M. TUBERCULOSIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2221;
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,662
FILING DATE: US-APR-1994
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Pred. No. 1.6e-
0; Mismatches
                                                                           TGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                                             951 CGCCATCGAGGTCGTATGGACGA 973
                                                                                                                                                                                                          Sequence 2, Application US/08228662 Patent No. 5688639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WGESSNER, WARREN D.
REGISTRATION NUMBER: 30,440
REFERENCE/FOCKET NUMBER: 150,3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WR-
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: MINNEAPOLI:
STATE: MINNESOTA
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Best Local S:
Matches 493
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                                                                                                                                                             Gaps
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                                                                                                                                     Length 2221;
                                                                                                                                                 Pred. No. 1.6e-79;
0; Mismatches 303; Indels
                                                                                                                                               . 6e-19
                                                                                                                                    Score 274.2;
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                                                                                                                                   Query Match 18.4%;
Best Local Similarity 61.4%;
Matches 493; Conservative
           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
612-305-1228
                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA
TELEFAX:
                                                                                                        US-08-852-219-2
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US-08-459-499-8

RESULT · 14

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APPLICANT: Young, Douglas B.
APPLICANT: Young, Douglas B.
TITLE OF INVENTION: Nucleic Acid Probes, Sequences, and Methods
TITLE OF INVENTION: Amended)
TITLE OF INVENTION: Amended)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: ADDRESS:
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                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.3 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,499
FILING DATE: 02-UNN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 274.2; DB 2;
Pred. No. 2.5e-79;
0; Mismatches 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE-TOCKET NUMBER: 03495.0110-03000
RELECOMMUNICATION INFORMATION:
TELECHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/875,940
FILING DATE: 30-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/929,206
FILING DATE: 27-MAY-1992
PRIOR APPLICATION NUMBER: US 08/029,655
FILING DATE: 11-MAR-1993
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 8, Application US/08459499 Patent No. 5871912 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         1300 I Street, N.W
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61.4%;
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Best Local Similarity 61.49
Matches 493; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                             Washington
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1346 TGGTGCAGCGTCTCCTGAAAATGTATTGGCGCCAGGGCCTGATGGTGCACCTGTGGAGGA 1405
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                                                                                                                                                                                                                                                           Length 4795;
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                                                                                                                                                                                                                                                       Score 274.2; DB 2;
                                                                                                                                                                                                                                                                       .5e-79;
les 303;
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                       NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 023
TELECOMMUNICATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                       18.48;
                                                                                                                                                                                                                                                                      llarity 61.4%;
Conservative
                                                                                          TELEFAN. (202) 408-4400
TELEFAN. (202) 408-4400
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                single
                                                                                                                                                              nucleic acid
                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 493; Conserv
                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                         MOLECULE TYPE:
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US-08-313-185-45
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                           2385 CCGACAACGCCAGCTTGGACAAGGCGCGCCGGCTGCTGTGGCCGGTCAAGAAGAAGTACG
                                                          GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAA--TGTTGCCCTTGAATC
                                                                                                                       CATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGAAGATGACTGGGAGTCGGACCT
                                                                                                                                       1286 CATGGATGATGAGGAGACTGTGGCCCTGATCGGGAGGGCATACATTTGGTAAAGCACA
CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACG
                                                                                                                                                                                GGTATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATAAAAACGGGAAAACT
                                                                                                                                                                                                           GGTCTATTGGGGCAAGGAAGCCACCTGGCTCGGCGATGACGGTTACAGCGTAAGCGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45, Application US/08313185
Patent No. 2851763
GENERAL INFORMATION:
APPLICANT: Heym. Beate
APPLICANT: Cole, Stewart
APPLICANT: Zhang, Ying
APPLICANT: Annore, Nadine
APPLICANT: Bodmer, Thomas
TILLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TILLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Finnegan, Henderson, Farabow, Garrett
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APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                         2325 ACGACGGCCGCGGCGCCGCGGGGGCGCATGCAGCGGTTCGCGCCGCTTAACAGCTGGC 2384
                                                               2743 CATGAACGACGTCGAAACAGCGGCGCTCGATCGTCGGCGCGCTCACATTCGGTAAGACCCA
                                                                                                                    988 GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAA--TGTTGCCCTTGAATC
                                                                                                                                                           2445 GCAAGAAGCTCTCATGGGCGGACCTGATTGTTTTCGCCGGCAACCGCTGCGCTCGGAATC
                                                                                                                                                                                                    1046 CATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTCGGACCT
                                                                                                                                                                                                                                                                              1106 GGTATACTGGGGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATAAAAACG
                                                                                                                                                                                                                                                                                                    1286 CATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGAGGGCATACATTTGGTAAAGCACA
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                                          928 CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                     1226 IGGAAAACCAGAICCICIGGCIICCGCGAAAGAIAICAGGGAAGCIITITCACGIAIGGC
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
GURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,887A
FILING DATE: 03-UL-1996
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALUNESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1466 TGCCTGGAAGGAGCCTGGTCGA 1488
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Patent No. 593300
GENERAL INFORMATION:
APPLICANT: Robertson, Dan E.
APPLICANT: Sanyal, Indrajit
APPLICANT: Adhikari, Robert S.
TITLE OF INVENTION: CATALASES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         688 ATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTC
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APPLICANT: Young, Douglas
APPLICANT: Young, Douglas
APPLICANT: Talang, Ying
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Rodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4795;
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ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.4%; Score 274.2; DB 3; Best Local Similarity 61.4%; Pred. No. 2.5e-79; Matches 493; Conservative 0; Mismatches 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02356.0068-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                              Sequence 45, Application US/09082614A
Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: HEYM, Beate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                   1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPRONE: (202) 408-4000
TELERAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meyers, Kenneth J
                                                                                                                                                                                Heym, Beate
Cole, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
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20005-3315
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                                                                                                US-09-082-614A-45
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CITY: Wa
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682 AATCAAATCCCTGGGGGGGTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGG 741
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                1441 GAAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGAC 1489
                                  24;
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15.1%; Score 224.6; DB 3; Length 2262;
Best Local Similarity 57.4%; Pred. No. 3.1e-63;
Matches 476; Conservative 0; Mismatches 329; Indels 24;
                                                                                                                                                                                                                                         BAIN, GILFILLAN,
& OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331400-55
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APPLICATION NUMBER: US/08/951,844
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICATION: 435
PRICA APPLICATION DATA:
APPLICATON DATA:
APPLICATON NUMBER: 08/674,887
FILING DATE: July 3, 1996
ATTONREY/AGRET INFORMATION:
NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                E: 3.5 INCH DISKETTE IBM PS/2
                                                                                                                        Sequence 5, Application US/08951844 Patent No. 6074860 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: Oligonucleotide US-08-951-844-5
                                                                                                                                                                     APPLICANT: Robertson et al.
TITLE OF INVENTION: Catalases
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE,
ADDRESSEE: CECCHI, STEWART
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEIC ACID
DEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                    CITY: ROSELAND
STATE: NEW JERSEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1261 TCAGGGAAGCTTTTTCACGTATGGCCATGGATGATGAGGAGACTGTGGGCCCTGATCGCGG 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAA 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAG 1380
                                                                                                                                                                                                                                                                                                                                                                                                    742 AGGCTCTGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGG 801
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                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                             Indels 24;
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                                                                                                                                                                                                                                                                           Score 224.6; DB 2; Length 2262;
Pred. No. 3.1e-63;
0; Mismatches 329; Indels 24;
                       09015/002001
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMUNICACION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2262 base pairs
TYPE: nucleic acid
STRANBEDNESS: double
                                                                                                                                                                                                                Coding Sequence 1...2259
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.4%;
Matches 476; Conservative
                                                                                                                                                                   linear
                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-674-887A-5
                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                          Length 2262;
                                                                                                                                                                         Score 224.6; DB 4; Length 2
Pred. No. 3.1e-63;
0; Mismatches 329; Indels
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                                                                                                                                                                      15.1%;
Best Local Similarity 57.4%;
Matches 476; Conservative (
                                                                                                             Coding Sequence 1...2259
              LENGTH: 2262 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
   SEQUENCE CHARACTERISTICS
                                                                               MOLECULE TYPE: CDNA
                                                                                                           ; NAME/KEY:
; LOCATION:
US-09-412-347-5
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                                                               AATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGAAGATGACTGGGAGTCGG 1101
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                                                                                   1102 ACCTGG---TATACTGGGGGCCTGACAACAAGCCTCTTGCAGAT----TATACTGGGGCCTGAACAACAAGAGCTCTTGCAGAT-----TATACTGGGGGCCTGAACAAGAGCCTCTTGCAGAT
                                                                                                                                           698 GCGACGTGAAAGCCAGAGACCATGGAAAAACCCGCTGGCGGCTGTCCAAATGGGTTTGA
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODFRATING SYSTEM: Windows95
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Fish & Richardson P.C.
1: 4225 Executive Square, Suite 1400
La Jolla
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09015/002001
TELECOMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ROBETSON, Dan E.
APPLICANT: Sanyal, Indrajit.
APPLICANT: Adhikari, Robert S.
TITLE OF INVENTION: CATALASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P
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APPLICATION NUMBER: 08/674,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09412347
Patent No. 6410290
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: METHOD FOR THE INTRODUCTION, OF GENETIC PARTHENOCARPY IN TITLE OF INVENTION: PLANTS
FILE REFERENCE: INTO GENETIC PARTHENOCAPRI IN PLANTS
CURRENT APPLICATION NUMBER: US/09/125,287B
CURRENT FILING DATE: 1998-11-09
EARLIER APPLICATION NUMBER: PCT/IL97/00051
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 6
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Pred. No. 0.045;
0; Mismatches 217; Indels
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                                                                                                                                        1085 RRRRRRRRRRRRRRRRATCGCAA 1060
                                                                                                      1425 AATAAATGTGGTACAGGAAACGGCAA 1450
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                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09125287B Patent No. 6114602 GENERAL INFORMATION:
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Patent No. 6114602
GENERAL INFORMATION:
APPLICANT: BARG, RIVKa
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SEQ ID NO 2
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Matches 169; Conservative
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US-09-125-287-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1125 AACAAGCCTCTTGCAGATAACGGGATAAAAACGGGAAACTTCAGAAACCTCTTGCCGCC 1184
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Best Local Similarity 3.1%; Pred. No. 5.6e-05;
Matches 12; Conservative 217; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                        Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                           STAIL.
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WOTTER: IBM PC COMPATIble
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APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
US-08-232-463-14/c
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SEQUENCE CHARACTERISTICS:
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                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98104-7092
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CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24
US-09-062-451-147/c
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APPLICANT: SALTS, Tehiam
TITLE OF INVENTION: METHOD FOR THE INTRODUCTION OF GENETIC PARTHENOCARPY IN
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 AAGTTGACTTTTGTATACAACATGCGAATTTCCCTTAATCCGGAGCTATTCGTATGATAA 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724 TTCAACAGCTGGATATGGAGGCTCTGAAAAAGATATCAAAGATTTGCTGACAACTTCCC 783
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Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12839;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.8; DB 3; Length 1
Pred. No. 0.083;
0; Mismatches 217; Indels
                                                         FILE REFERENCE: INTRO GENETIC PARTHENOCAPRI IN PLANTS CURRENT APPLICATION NUMBER: US/09/125,287B
CURRENT FILING DATE: 1998-11-09
EARLIER APPLICATION NUMBER: PCT/IL97/00051
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1
LENGTH: 12839
                                                                                                                                                                                                                                                                                                                ; NAME/KEY: unsure
; LOCATION: (5)..(11322)
GOTHER INFORMATION: "n"'s are any nucleic residue
US-09-1125-287-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4187 TGTATACCAACATTATGTAATATGAT 4212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: TPRP-F1 GENOMIC CLONE
                                                                                                                                                                                                                                                                                                                                                                                                                     2.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similaria,
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
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Best Local (
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1316 CGCGGGAGGCCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGG 1375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGACATCATCACCGTGTACCAGCAGAAGGTGGAGGACGTGG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.3%; Score 33.8; DB Best Local Similarity 57.8%; Pred. No. 0.57; Matches 59; Conservative 0; Mismatches
                                                                                        APPLICATION NUMBER: US/08/991,789A FILING DATE: 11-Dec-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 147:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210121.41902
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 147, Application US/09062451
Patent No. 6344550
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 147:
                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-1997
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Sequence 5, Application US/08716351A
Patent No. 6033905
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 1521
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%;
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LENGTH: 10970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
COCATION: 1..10970
OTHER INFORMATION: /sta
COTHER INFORMATION: vect
US-08-716-351A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 77; Conserve
                                                                                             GENERAL INFORMATION:
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                                           US-08-716-351A-5/c
                                                                                                                  APPLICANT:
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                                                                                                                                                        1316 CGCGGGAGGGCATACATTTGGTAAAGCACCATGGTGCAGCGTCTCCTGAAAAATGTATTGG 1375
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                                                                                                                                                                            1316 CGCGGGAGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGG 1375
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                             ö
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ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Sulte 6300
                                                                                    Score 33.8; DB 4; Length 579;
Pred. No. 0.57;
0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 579;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1376 CGCAGGGCCTGATGGTGCACCTGTGGAGGAGCAGGGACTGGG 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Potter, Jane E.R.
REGISTRAILON NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.41901
TELECOMMUNICATION INFORMATION:
                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33.8; D
Pred. No. 0.57
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       Sequence 147, Application US/09598326 Patent No. 6423496 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                      2.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.3%;
Best Local Similarity 57.8%;
Matches 59; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Washington
                                                                                                                        Conservative
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ZIP: 98104-7092
                  single
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TYPE: nucleic acid
STRANDEDNESS: sing
                                   linear
                                                                                                   Local Similarity
nes 59; Conserv
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US-09-598-326-147/c
                                                  US-09-062-451-147
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                                                                                      Query Match
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Matches
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Sequence 2054, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICART: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: ETIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1267 AAGCTTTTTCACGTATGGCCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGAGGGC 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1327 ATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGCCTG 1386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name= "p537 retroviral vector"
Gibbon Ape Leukemia Virus-Based
Retroviral Vectors
                                                                                                                     COMPUTER: IBM TO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33.8; DB 3;
Pred. No. 3.3;
0; Mismatches 72;
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15280-128-1PC
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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RESULT 30
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                                                                                                                                                                                                                                                                                                                      557 ACTCCTCTGAGATTACACAGCCCTGAATCAAATCCCTGGGGGGCTGATTTTGATTATGCC 716
                                                                                                                                                                                                                                                                                                                                                     838 TATATCGTGAGGTTAAACTTTACTGGTGAAATACGACTGAGCCTATCATATCTTATATG 897
                                                                                                                                                                                                                                                                                778 GATITAAACGAIGAITITGAAGAITCITIAGAGIATITGGAGCCAITAGAICAIGAIGCA 837
                                                                                                                                                                                                                                             597 GCTGTAGCCGCTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTA
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                                                                                                                                                                     Score 33.4; DB 4; Length 1074; Pred. No. 1.1; 0; Mismatches 86; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Seellg, Hans Peter
APPLICANT: Renz, Hans Peter
APPLICANT: Renz, Hans Peter
TITLE OF INVENTION DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0030-599
CURRENT APPLICATION NUMBER: US/08/913,832A
CURRENT APPLICATION NUMBER: PCT/DE96/00444
PRIOR PLILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-03-08
NUMBER OF SEO ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 6.9;
0; Mismatches 81;
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674-
SEQ ID NO 2054
LENGTH: 1074
                                                                                           ; TYPE: DNA; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08913832A Patent No. 6329517
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85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(5736)
US-08-913-832A-1
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SEQ ID NO 1
LENGTH: 6328
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Best Local 9
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Matches 8
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Fabrics Using Truncated
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APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0059-999
CURRENT APPLICATION NUMBER: US/09/249,181A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/913,832
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1996-01-12
PRIOR FILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellulase Enzyme Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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Glbbs, Moreland
Bergquist, Peter
Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
TITLE OF INVENTION: Treating Cellulose Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.4; DB Pred. No. 6.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/136,574A FILING DATE: 19-Aug-1998 CLASSIFICATION: <UNKNOWN> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/932,571 FILING DATE: September 19, 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graham K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-136-574A-1/c
; Sequence 1, Application US/09136574A
; Patent No. 6294366
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
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ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Farrington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.0
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: CDS
) LOCATION: (1)...(5736)
US-09-249-181A-1
                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 6328
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Length 43795;

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40803 AIGICIGCCIAACIACCIAIGGIAACAAAGCITITITITITITITITITIGAGGCAA 40862
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                                                                                                                                                                                                                                                                                                                  847 GTGCCGGAACATACAGGACATATGATGGCCGGGGGGGGCGCCAGTGGTGGTGGTCAGCAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                  40923 AACCICCAGGGCICAATIGAICCICCCACCITAGCCICCIGAGIAGCCAGGACTACGGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         967 GGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTG
                                                                                                                                                                                                                                                                                                                                                                          907 ITGAACCGCTGAACAGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1027 GTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCTGGC 1076
                                                                                                                   Score 32.4; DB 3; Length 4
Pred. No. 22;
0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: DeBoff, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Comparatible
OMPUTER: IBM Comparatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08804227C Patent No. 5876991
                                                   MOLECULE TYPE: DNA (genomic)
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TELECOMMUNICATION INFORMATION
                                                                                                                 Query Match 2.2%;
Best Local Similarity 44.5%;
Matches 129; Conservative
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
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               single
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350..14002
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STRANDEDNESS: single
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           STRANDEDNESS:
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                                                       ; MOLECULE TYP
US-08-742-185-101
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      440 IGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAAGTTGACTTTTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1841 ATCAGAGGCAATGCTTTTGTAAGACAAAGCTACTTTGAAATAATCTCT 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Page, David C.
APPLICANT: Reljo, Renee
APPLICANT: Reljo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Bawkins, Trevor
APPLICANT: Reeve, Mary Pat
TILE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                             Length 11707;
                                                                                                                                                                                                                                                                                                                                                                   51; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                             DB 4;
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
                                                                                                                                                                                                                                                                                                                      Score 32.4; DB Pred. No. 10; 0; Mismatches
                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-UUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07A2
TELECHMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 101;
                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101, Application US/08742185 Patent No. 6020476 GENERAL INFORMATION:
                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      Ouery Match 2.2%;
Best Local Similarity 55.3%;
Matches 63; Conservative
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nucleic acid
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31606 CAGTACGAGGTGCCGGGCGTGTCGGGGTCGGGCGAGTACCTTCCCTCCACGTCCCAGCCG 31547
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                                                                                                                                                                                                                                                                                                                                                                      167 GGGAAGCATCAGAAGGCCGGGGAACTCCGTCCGGCCAGTGAACCGTGCCACACTCCGGG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 CCTTAGTATTTTTTGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCA-A 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 AAAAAAAACTCTTCCTGTTCTGATTCTTCTGCGCGTATCGGGGGAGCTTTTCTACCGCTGT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                               227 CAGTACATGCCGCCGCGCGCTGATACCGGCAAGAATGGTCGCAAACTCCCGCTCCGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bernstein, Harold S.
APPLICANT: Coughlin, Shaun R.
TITLE OF INVENTION: Mathods and Compositions for Regulating Cell Cycle
TITLE OF INVENTION: Progression
FILE REFERENCE: UCSF-020/01US
CURRENT APPLICATION NUMBER: US/09/156,316
CURRENT APPLICATION NUMBER: 60/060,688
EARLIER APPLICATION NUMBER: 60/060,688
EARLIER FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                  Length 44377;
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0; Mismatches 105;
                                                                                                                                                                                                                                                                                                  DB 2;
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Pred. No. 26;
0; Mismatches
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50.0%; Pred. No. 9
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Patent No. 6183961
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              Query Match 2.2%;
Best Local Similarity 53.6%;
Matches 67; Conservative
                                                         CDS
14046..20036
                                                                                                                                                                    CDS
31329..36071
                                                                                                                                                                                                                                          36155..41830
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Matches 106; Conservative
                                                                                                            CDS
20110..31284
   CDS
350..14002
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
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; LOCATION:
US-08-804-198-1
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                                                                                                                                                                                                                                                            Length 44377;
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APPLICANT: Rubstoss, Stuart A.
APPLICANT: Richardson, Mark A.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
ITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
SFREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                        Query Match 2.2%; Score 32.2; Di
Best Local Similarity 53.6%; Pred. No. 26;
Matches 67; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPETWARING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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36155..41830
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                                    14046..20036
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31329..36071
                                                                                       20110..31284
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CGGTC 31542
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               NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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US-08-804-227C-7
                                                                                                                                                                                   NAME/KEY:
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STATE:
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FEATURE
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286

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2401 AGCCTCCGGGGAATAGCAGAATCTTCATGTTT 2370

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1110 TACTGGGGCCTGACAACAAGCCTCTTGCAG 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-09-196-390-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                        APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2060 GGAGTICCAAGGATGGTATICACCGGCGAAATCGCCGATGACGAGGAGAAATCATACA 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 TATTICAGGATACCCTICGICAICAACACGTACAAACCAGAAGACCAGCTITITGTITCT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618 TATTACAGAATTGTCAACCTCATGAAGAAAGAACGTGCAGAACGAGAGCTTTATGTCGAT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: VAKHARIA, Vikram ,

APPLICANT: YAO, Kun

TITLE OF INVENTION: METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS

TITLE OF INVENTION: PANCREATIC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA

TITLE OF INVENTION: TRANSCRIPTS

FILE REFERENCE: 8288-9023

FILE REFERENCE: 8288-9023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 2278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 31.8; DB 4; Length 3097;
59.3%; Pred. No. 7;
tive 0; Mismatches 37; Indels 0
                                                                                                                              APPLICANT: Andersen, Jens Tonne
APPLICANT: Andersen, Jens Tonne
APPLICANT: Andersen, Stanislase Dusko
TITLE OF INVENTION: No. 6306631e1 ppGpp Synthetase and Exp;
TITLE OF INVENTION: Systems for Improved Production of Proj
FILE REPERBENCE: 5259.204-US
CURRENT APPLICATION NUMBER: US/09/442,055
CURRENT FILING DATE: 1999-11.16
FARLIER PILING DATE: 1997-06-20
NUMBER OF SEQ ID ANS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 GACATCCACAAAGAAGGGAATATTCAGGTCTGCGCAGCA 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31.8;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application US/09282147 Patent No. 6274147
                                                                      Sequence 1, Application US/09442055 Patent No. 6306631 GENERAL INFORMATION:
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Best Local Similarity 57.6%;
Matches 57; Conservative
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Best Local Similarity 59.3%
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS
) LOCATION: (21)...(2222)
US-09-442-055-1
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: relA-bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-282-147-38
                                                US-09-442-055-1
                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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NUCLEIC ACID MOLECULES ENCODING ENZYMES FROM WHEAT WHICH ARE INVOLVED IN STARCH SYNTHESIS
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ZIP: 10020
COMPUTER READBLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/196,390
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED INTILE OF INVENTION: SYNTHESIS
TITLE OF INVENTION: SYNTHESIS
TURBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave STREET: 1251 Avenue of the Americas
2120 ATCTGCGGTGTAGACATCAAAGCCATCGCAG 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: CDNA library in pBluescript sk (-) CLONE: pTASS1
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APPLICATION NUMBER: DE 196 21 588.9
FILING DATE: 29-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 11-SEP-1996
PRIOR APPLICATION NUMBER: PCT/EP97/02793
APPLICATION NUMBER: PCT/FP97/02793
ATTORNEY AGENT INFORMATION:
NAME: HALEY, JT., JAMES F.
REGISTATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: AGREVO-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: cv. Florida
TISSUE TYPE: ca. 21 d Caryopses
                                                                                               US-09-196-390-5; Sequence 5, Application US/09196390; Setent No. 6307125; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum L.
                                                                                                                                                                                                                        Lorz, Horst
Lutticke, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                APPLICANT: Walter, Lennart
APPLICANT: Frobberg, Claus
                                                                                                                                                                                               Block, Martina
                                                                                                                                                                                                                                                                                                                  APPLICANT: Kossmann, Jens
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162..2559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
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1270 CTTTTTCACGTATGGCCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGCATA 1329
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2852 TCTCCCACACAGAAGACATCACAGGCTGCCTTGAAGACCTTCTTGGCCCAGGTCCTGA 2795
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Pred. No. 10;
0; Mismatches 54; Indels 0
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                                                                                                                                                                                                          APPLICANT: Bishopric, Namette H.
APPLICANT: Murphy, Birlan
Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
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ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         Sequence 18, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 324-0880
TELEFRA: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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Similarity 54.2%;
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 350 Camb
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94306
                                                                                                     US-08-880-342-18/C
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US-08-880-342-18
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Best Local
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                                                                                                   1212 CCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCT 1271
                                                                                                                                          918 CCTGCAGCCCCCGCTGTACAAGAACCTTTGGGATTTCAAGAAATACATTGGTTTCGAG 977
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                                                             Gaps
                                                                                                                                                                                                            1272 TTTTCACGTATGGCCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGG 1321
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                 Score 31.6; DB 4; Length 2825;
Pred. No. 7.7;
0; Mismatches 49; Indels 0
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tive 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Deblinger & Associates
STREET: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human NOS-1 gene, Fujisawa,
J. Neurochem 63:140 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1994
                                                                                                                                                                                                                                                                                                               US-08-365-486A-18/c
; Sequence 18, Application US/08365486A
Patent No. 5834306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 1.2.
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/POCKET UNBERE: 38,515
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base_pairs
                   2.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
               Query Match 2.19
Best Local Similarity 55.5
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94306
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STATE:
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Sequence 3, Application US/09123624

Patent No. 6149936

GENERAL INFORMATION:
APPLICANT: SCHRADER, Jurgen
APPLICANT: GODECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2004
CURRENT APPLICATION NUMBER: US/09/123,624
CURRENT APPLICATION NUMBER: US/09/123,624
CURRENT APPLICATION NUMBER: 08/553,503
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SECTIONER OF SEQ ID NOS: 6
SECTIONER OF SEQ ID NOS: 6
SECTIONER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1270 CTTTTTCACGTATGGCCATGGATGATGAGGACTGTGGCCCTGATCGCGGGGGGCCATA 1329
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                    INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC INVENTION: TREATMENT OF VASCULAR DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                Length 4780;
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Pred. No. 11;
0; Mismatches
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Pred. No. 11;
0; Mismatches
                                                                          CURRENT APPLICATION NUMBER: US/09/123,708
CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: P4411402.8
EARLIER FILING DATE: 1994-03-31
NUMBER OF SEO ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                         2.1%;
ilarity 54.2%;
Conservative
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             TITLE OF INVENTION: DNA EXPR
TITLE OF INVENTION: TREATMEN
FILE REFERENCE: 511169-2003
                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Cytomegalovirus
US-09-123-708-3
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local Simil
Matches 64; C
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  2852 TCTCCCACACAGAAGACATCACAGGCTGCCTTGAAGACCTTCTTGGCCCAGGTCCTGA 2795
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FEBS Lett 316:175 (1993)
                                                                                                                                                                        APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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Pred. No. 11;
0; Mismatches
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NAME: Sholtz, Charles K.
REGISTATION NUMBER: 38,615
REFRENCE/DOCKET NUMBER: 8255-0018
TELEPONE: (415) 324-0800
TELEPHONE: (415) 324-0800
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                          Sequence 20, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09123708
Patent No. 6146887
GENERAL INFORMATION:
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Best Local Similarity 54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4780 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 431..4732
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HYPOTHETICAL: NO
ANTI-conne
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                                                                                                                                                                                                                                                                                                                                                                                                USA
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                  94306
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US-09-123-708-3/c
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STATE:
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1119 TGCAGCAGCGCCTGGGGCGGGAGGAGGAGAAGATCAAGCAGCCGCACCGTAAGTACC 1178
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US-09-007-005-17
Sequence 17, Application US/09007005B
Fatent No. 628658
Jeacht No. 628658
Jeacht No. 628658
Jeacht Soberts, Jack W.
Jepticant: Liu, Richard W.
APPLICANT: Edu, Richard W.
APPLICANT: Liu, Richard W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1999-01-14
EARLIER FILING DATE: 1999-01-14
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
SEARLIER FILING DATE: 1999-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FatlsEQ for Windows Version 4.0
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0; Mismatches
  FITLE OF INVENTION: CDK4 Binding Proteins UMBER OF SEQUENCES: 95
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                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NOWBER: US/08/253,155A
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION UNDABER: MII-028
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                            ....rESSEE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston STATE: MA COUNTRY: USA
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Best Local Similarity 51.8
Matches 71; Conservative
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STRANDEDNESS: sing
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                                               APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: Dalo Alto
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: '23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 0.14

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/ABENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFRENCE/DOCKET WINDER: 38,615
REFRENCE/DOCKET WINDER: 38,615
REFRENCE/DOCKET WINDER: 38,615
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARRACTERISTICS:
LENGTH: 4780 base pairs
LENGTH: 4780 base pairs
TENGTH: 4780 base pairs
TENGTH: 4780 base pairs
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Patent No. 5691147
Bishopric, Nanette H.
Murphy, Brian
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APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
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COMPUTER READABLE FORM:
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431..4732
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Matches 64; Conserva
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ORIGINAL SOURCE:
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US-08-880-342-20
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Patent No. 6312921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/09341678
; Patent No. 6252138
; GENERAL INFORMATION:
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Best Local Similarity 45.0%;
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Patent No. 6281344

GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Szostak, Richard W.
APPLICANT: LIV. Ribe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: 1991000

CURRENT FILING DATE: 1999-02-05

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-06

EARLIER FILING DATE: 1997-11-06

EARLIER FILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 33

SOFTWARE FEASTSEQ for Windows Version 4.0
                                                                                                                                                                          Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1431 TGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGG 1473
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                                                                                                                                                                     tch 2.1%; Score 31; DB 4; Length 289 al Similarity 4.9%; Pred. No. 3.1; 11; Conservative 95; Mismatches 117; Indels
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Best Local Similarity 4.9%; Pred. No. 3.1;
Matches 11; Conservative 95; Mismatches 117; Indels
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                     FEATURE: OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Translation template
                                                                       NAME/KEY: misc_feature
LCCATION: (1)...(289)
CTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
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: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A/T,C or G

US-09-244-796-17
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 17
LENGTH: 289
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Best Local
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2661 CCAGTGCTGTCCCTCAAGAGGAAGCGACCCCTCAGTCACACCAGCGGAAGAGATGGGTG 2720
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APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallide, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Werberg, David
APPLICANT: Wishard Genetics Institute, Inc.
APPLICANT: Werberg, Sia
APPLICANT: Werberg, Sia
APPLICANT: Maurice
APPLICANT: Maurice
APPLICANT: Momentiant Schereb
APPLICANT: Genetics Institute, Inc.
APPLICANT: Publicant Schereb
CURRENT APPLICANTION NUMBER: US/09/175,928A
CURRENT APPLICANTION NUMBER: US/09/175,928A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 ACTCCGTCCGGCCAGTGAACCGTGCCACACTCCGGGCAGTACATGCCGCCGGCGCTGATA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CCGGCAAGAATGGTCGCAAACTCCCGCTCCGTGCAGCGGGCTATTTCAGGATACCCTTCG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 TCATCAACACGTACAAACCAGAAGACCAGCTTTTTGTTTCTGACATCCACAAAGAAGGGA 370
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                                                                                                                1431 TGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGG 1473
                                                                                                                                                 Indels
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APPLICANT: BARTHELS, Nathalie
APPLICANT: GHESTSEN, Gadelieve
TITLE OF INVENTION: PATHOGEN-INDUCED PLANT PROMOTERS
FILE REFERENCE: 6201-0014
CURRENT APPLICATION NUMBER: US/09/341,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30.8; DB 4;
Pred. No. 15;
0; Mismatches 142;
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4113218 CAGTGACGGTCGGCGATGCGGGCCGTACAACATCTGACCGGGATCCGGCTATTGGGC 4113277
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CHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
GS-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                    NAME/KEY: MAKARI7
LOCATION: 945..968
OTHER INFORMATION: region corresponding to oligonucleotide MAKARI7
FEATURE:
NAME/KEY:
LOCATION: 1444..1445
OTHER INFORMATION: Insertion point of T-DNA
OTHER INFORMATION: Insertion in the line ARMI
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Pred. No. 18;
0; Mismatches 47; Indels
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. LOCATION: 1418..1570

. OTHER INFORMATION: putative open reading frame US-09-341-678-5
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Pred. No. 67;
0; Mismatches
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: PCT/EP98/00388
EARLIER FILING DATE: 1998-01-19
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%;
Best Local Similarity 55.7%;
Matches 59; Conservative
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ilarity 57.1%;
Conservative
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Matches 56; Conserve
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LENGTH: 4403765
                                                                                                                               LENGTH: 4160
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                                                                               APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PUBERS. Obn C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007,00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4121083 ACAAGCCAGTTCCTATTGGGCACAAGCCAATTAGAAAT 4121120
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                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
COTHER INFORMATION: H37Rv
US-09-103-840A-1
                  Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.19
Best Local Similarity 57.19
Matches 56; Conservative
                                                                   GENERAL INFORMATION:
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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BG370112 LmA123 VB AL144438 Anopheles AW180683 MgA0831f BG278355 a39G3np.r BD412683 113 Metar BH403595 AG-MD-127 AW180185 MgA0268f AW180185 MgA0268f AW1802076 mgap0008xD BM86928 mgns008xE BF750228 mgns008xE BF750228 mgns0014xP BW86928 mgns0002xC BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108473 BF739529 NCM108673 BF739529 NCM108673 BF762769 BW8A07396 BF762769 BW8A07396 BF762769 BW8A07396 BF762769 BW8A07396 BF762769 BW8A07396 BF762769 BW8A07396 BF79229 RF711-5114 BF495230 AT04106.5 BF63531 PAN PAN PAN PAN PAN PAN PAN PAN PAN PAN	A2978404 2M024816 AJ454978 AJ454978 BG387766 602412644 BG3320813 BNISC_mql4 BG322881 EMI_15_CO AL098749 Drosophil AL098749 Drosophil AC59871 Drosophil AC59871 Drosophil AC59871 Drosophil AC59871 Drosophil AC59871 AC600244 BE874869 601488919 AX108097 Zea mays W09301 mag3400.r1 AZ723610 RPC-24-6 BH401331 AG-ND-137
1.8 562 12 BG370112 0.8 573 10 AM180683 0.0 4 65 12 BG3701112 0.0 573 10 AM180185 0.0 571 10 AM180185 0.0 571 10 AM180185 0.0 571 10 AM180185 0.0 571 10 AM180185 0.0 10 AM180185 0.0 571 10 AM180185 0.0 10 AM180185 0.0 10 AM180185 0.0 10 AM180185 0.0 10 AM180185 0.0 10 AM180185 0.1 14 BM665076 0.1 14 BM665078 0.1 14 BM665078 0.1 14 BM665078 0.2 14 BM66508 0.3 17 14 BM66508 0.3 17 14 BM78213 0.4 14 BM78213 0.5 10 AM79213 0.6 10 AM79213 0.7 10 AM780185 0.8 11 10 BM78213 0.8 11 10 BM78213 0.9 11 BM78213 0.0 10 AM79213 0.0 10 A	702 17 4 4 835 9 4 633 14 4 1051 17 4 1101 17 4 1115 112 4 2321 111 4 555 17
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S.1.6 Compugen Ltd. earch time 1574.88 Seconds (without alignments) 15312.305 Million cell updates/sec. 15312.305 Million cell updates/secctggaaggagcctggtcgac 1489 meters: 32308132 s	results predicted by chance to have a to the score of the result being printed, of the total score distribution. SUMMARIES ID Description BQ752115 BQ752115 BQ751180 BQ751181 BQ751181 BQ751181 BQ751181 BQ751181 BQ751181 BQ751181 BQ751181 BQ7511881
Genc Copyright (c) 1 June 18, 2003, 01 June 18, 2003, 01 June 18, 2003, 01 L ctgcagtccggagat L ctgcagtcggagat L ctgcagatcggagat L ctgcagatcggagatcggagat L ctgcagatcggagat L ctgcagatcggagatc	## the number of sater than or equal srived by analysis ## Query Match Length DB 13.2 707 14 13.2 707 14 12.8 639 14 12.4 742 14 12.4 742 14 12.4 742 14 11.9 729 10
OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Searched: Total number of Minimum DB seq lu Maximum DB seq lu Maximum DB seq lu Database:	Pred. No. score gree and is de and is de No. Score 196. 3 197. 2 196. 3 191. 4 185. 2 5 183. 2 6 176.8

us-09-674-277-1.rst

ALIGNMENTS	BQ752115 EST633278 DSCT Colletotrichum trifolii cDNA clone pDSCT10-12, mRNA	Sequence: B0752115.1 G1:21907520 BST: C011cttibue A./6211	Collectrichum trifolii. Collectrichum trifolii. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; incertae sedis; Phyllachorales; Phyllachoraceae;	<pre>mitosporic Pnyllachoraceae; Colletotrichum. 1 (bases 1 to 762) Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,</pre>	Cheung, F. and Fraser, C.M. ESTS from mycelia of Colletotrichum trifolii race 1 Unpublished (2002) Other Rere. Fere, Fere, 73777	Contact: Deborah A. Samac Contact: Deborah A. Samac Department of Plant Pathology University of Minneseta	495 Borlang Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 625 1243	Fax: 0.21 04: 0.25 0.05 Email: debbys@puccini.crl.umn.edu TIGR sequence name: MTSAJ12TV More information is available at:	Seq prin		/db_xref="taxon:5466" /clone="pbSCT10-12" /clone 1 th="nec"	/tissue_type="mycelia" /dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minima) medium		/notes vector: pHinescript SR+; Site_1: EcoRI; Site_2: ECORI; isolate: 2582; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into Lambda gill from	Stratagene and packaged using Gigapack packaging extracts. An allquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was usurified from a limid	lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into paluescript SK+. Aliquots of the ligation were used to transform E. coli pH5alpha which	were plated onto medium with X-gal for selection of recombinants." 163 a 267 c 221 g 111 t	13.28:	Similarity 62.2%; Pred. No. 4.3e-51; 0; Conservative 0; Mismatches 188; I		CTGGGGGGGTGA TTTTTGA TTTTTGA TOTAL COLOCGC CAGCA CAGCA CAGCA CAGCA CCC CGTCA CCAACCC		752 AAAAGATATCAAAGATTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATGGTCA 811	272 GAAGGACCTCACGGCCCTGATGACCGACTCCCAGGACTGGTGGCCTGCCGACTTTGGCCA 331
	RESULT 1 BQ752115 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT				FEATURES								BASE COUNT	ORIGIN Query Match	Best Local Matches 3	Oy 40				Dp 3
AA739503 268 PLIFG AZR96697 PBTT-34-2	ALOSONO METAL 24-2 BH158931 ENTOS6FTF BG964409 602832052 ALO52823 Drosophil ALS61266 ALO561266 AW882293 CM0-0T005 AW608791 QY2-PT001	AQ567331 HS_2110_B AL366725 MTBAO9G07 BJ295668 BJ295668 AZ327913 IMO051M06	A1908795 QV-BT191- AZ56307 258PvG10 WZ7996 43ez Human A1.07630 prosophil	A1057674 TENUT764 AV252655 AV252655 AA34804 ERT63324	BE976970 B58407.y BG157767 saa89403. BE233807 140289 MA	BG212271 RST31855 BGG35053 AT31512.5 BH156360 ENTSM61TF	AL582541 AL582541 AZ546952 ENTDP10TF AL417818 T7 end of	Drosop AGENCOL RPCI - 2	BB554095 BB554095 AW081507 xc42b03.x BG899691 HOA39-1-D	BM288646 529986 MA BH024692 RPCI-24-3	AW271670 xs10g04.x AL659013 AL659013 BH715498 BOMGP70TF	B0849666 QGB10102. B0854322 QGB22024. BQB55297 QGB25M05.	AL234371 Tetraodon BH664387 BOMIK81TR AL064465 Drosophil	AL109147 Drosophil BF677027 602084262 AK017959 Mis miscu	AI728141 BNIGH1950	BB205464 BB205464 AZ190971 SP_1018_B AL150863 Anopheles	AE011067 AE011067 AL519510 AL519510 AZ542487 ENTEBLIR PIEC1776	ALOSB396 Drosophil ALOSB396 Drosophil ALIO3208 Drosophil	ALO76421 Drosophil ALO76504 Drosophil AA834443 of68f09.r	BM660332 952036G07 AW265830 L30-2553T BM661250 952046B07	BM661249 952046B07 AU039069 AU039069	AI612529 TENGO325 BJ080416 BJ080416 AZ001002 RPCI-23-3	AZ330097 1M0055G10	_
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/dev_stage="xoung, actively growing mycelia (3 days after incoulation) grown in liquid culture (cutin minimal medium containing 2%qucose)."
/lab_host="DH5alpha"
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EST632364 DSCT Colletotrichum trifolii cDNA clone pDSCT7-68, mRNA
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Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli T1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
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Colletotrichum trifolii
Eukaryota; Fungl. Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 707)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,
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Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108,
Tel: 612 625 1243
Fax: 651 649 5058
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TIGR sequence name: MTSAG68TV More information is available at:
www.medicago.org
                                                                                               TTATGGTCCTTTCTTTATTCGTATGCCTTGGCACGGTGCCGGAACATACAGGACATATGA
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ESTs from mycelia of Colletotrichum trifolii race
Unpublished (2002)
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Other_ESTs: EST632074
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Fax: 651 649 5058
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1 (bases 1 to 639)
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Fraser,C.M.

ESTs from mycelia of Colletofrichum trifolil race 1
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/organism="Colletotrichum trifolii"

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Location/Qualifiers
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ilarity 62.0%;
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                                                                                                                                                                                  /tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after incolation) grown in liquid culture (cutin minimal medium containing 28qucose)."
                                                                                                                                                                                                                                                                     Anote—"Vector: pBluescript SK+; Site_1: ECORI; Site_2: BCORI; Slolate: 2925; CDNA was prepared from polyatenriched RNA The CDNA was ligated into Lambda gtll from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli X1090 and phage DNA was purified from a liquid lysate. The CDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+ Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of
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EST652444 DSCT Colletotrichum trifolii cDNA clone pDSCT8-27, mRNA
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Best Local Similarity 64.2%; Pred. No. 3.8e-49;
Matches 287; Conservative 0; Mismatches 160; Indels
                                                                                                    /organism="Colletotrichum trifolii"
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Location/Qualifiers
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   debbys@puccini.crl.umn.edu
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                                                                                                                                   /db_xref="taxon:5466"
/clone="pDSCT5-66"
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                                                                                                                       /strain="race 1"
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Email: debbys@puc
TIGR sequence nam
                                                    Sed primer:
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Unpublished (2002)
Other_ESTs: EST632443
Contact: Deborah A. Samac
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAH27TV More information is available at:
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/dev_stage="Young, actively growing mycelia (3 days after incolation) grown in liquid culture (cutin minimal medium containing 28quose)."
/lab_host="DH5alpha"
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COR1; isolate: 28p2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtil from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The CDNA inserts were gel purified after EcoR1
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DHSalpha which
were plated onto medium with X-gal for selection of
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Colletotrichum trifolii.
Colletotrichum trifolii
Eukaryota; Rungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.

1 (bases 1 to 742)
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,
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                                                                                                                                                                                                                 Cheung, F. and Fraser, C.M. ESTs from mycelia of Colletotrichum trifolii race 1
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691

Indels

1.1e-46; thes 173;

Pred. No. 1.1e-0; Mismatches

194

751

254

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374 930 434 990

871

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991 CCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGG 1050
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  63.1%;
Best Local Similarity 63.1
Matches 298; Conservative
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ECORI: isolate: 28p2 ; CDNA was prepared from polyA-
ECORI: isolate: 28p2 ; CDNA was prepared from polyA-
ECORI: isolate: 21p2 ; CDNA was ligated into Lambda gtil from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The CDNA inserts were gel purified after ECORI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DHSalpha which
were plated onto medium with X-gal for selection of
                                                                                                                                                                                                                                                                                                                                                                       EST631950 DSCT Colletotrichum trifolii cDNA clone pDSCT4-87, mRNA sequence.
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/dev_stage="Young, actively growing mycelia (3 days after incolation) grown in liquid culture (cutin minimal medium containing 2&quocse)."
/lab_host="DH5alpha"
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                     GATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACGGC 989
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1 (bases 1 to 606)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.

ESTS from mycella of Colletotrichum trifolli race, 1
Unpublished (2002)
Other_ESTS: EST631951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaud Hall, 1991 Upper Buford Circle, St. Paul,
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TiGR sequence name: MTSAD87TK More information is ava
www.medicago.org
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
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/db_xref="taxon:5466"
/clone="pDSCT4-87"
/clone_lib="DSCT"
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AW179968 729 bp mRNA linear EST 17-NOV-1999 MGA0020f MGA Library Mycosphaerella graminicola cDNA clone MGA0020 5' similar to catalase-peroxidase, mRNA sequence.
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/strain="Strit"
/db_xref="taxon:54734"
/clone="Mah0020"
/clone=llb="Mah Library"
/note="Vector: pSPORT1; Library constructed from cultures
utilizing ammomium ions as a source of nitrogen"
                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
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Keon, J. P. R. Balley, A. M. and Hargreaves, J. A.

A group of expressed cDNA sequences from the wheat fungal leaf
Blotch pathogen, Mycosphaerella graminicola (Septoria tritici)
20374020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Biology Department
IACR-Long Ashton Research Station
IACR-Long Ashton, Bristol, BS41 9AF, UK
Tel: 444(0)1275 392181
Fax: +44(0)1275 394281
Email: john.nargreaves@bbsrc.ac.uk
Insert Length: 2600 Std Error: 0.00
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                       Mycosphaerella graminicola.
Mycosphaerella graminicola
                                                                                                                       AW179968.1 GI:6447163
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12.3%; Score 183.2; DB 14; Length 606;

Query Match

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AL144438.1 GI:7002600
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Genoscope.
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267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            992 CAGTATITCCIGGGGAGACCIGAIGGICCIGACIGGIAAIGIIGCCCIIGAAICCAIGGG 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                             1052 ATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAAGTCG---GACCTGGT 1108
                                                                                      632 CTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATTACACAGCCCTGAATCAAATCC 691
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                                                                                                                                                       CTGGTGGCCAAATGAGCTGAACACCAAGATCCTGCGCCAGCACCACCGCTGCTACCGACCC
                                                                                                                                        CIGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTCTGAA
                                                                                                                                                                                         752 AAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATGGTCA
                                                                                                                                                                                                                                                                                            TGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGCCGGA
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                                                                     Gaps
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1 (bases i Lo 562)

1 (dases i Lo 562)

1 (dases i Lo 562)

Expressed sequence tags of Leptosphaeria maculans, cause of blackleg disease of oilseed Brassicas
Unpublished (2001)

Contact: Alexander Idnurm

Barbara J. Howlett (bhowlett@unimelb.edu.au)

School of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The University of Melbourne, Parkville, VIC, 3010, Australia
Tel: 61 3 8344 5056
Fax: 61 3 9347 5460
                                                                   3;
                                          DB 10; Length 729;
                                                                   Indels

    562
/organism="Leptosphaeria maculans"

                                         Score 176.8; DB 10;
Pred. No. 1.4e-44;
0; Mismatches 192;
     150 t
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Insert Length: 2700 Std Error: 0.00
Seq primer: T3 Universal Primer.
Location/Qualifiers
      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                blackleg of rapeseed fungus.
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   203
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EST.
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                                       tch 11.9%;
al Similarity 61.0%;
305; Conservative
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  217
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                                      Query Match
Best Local S
Matches 305
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BASE COUNT
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Anopheles gambiae GSS SP6 end of clone 08MO5 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                           686 AAATCCCTGGGGGGGTGATTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGC 745
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2 (bases 1 to 737)
2 (bases 1 to 737)
3 (bases 1 to 737)
4 (bases 1 to 737)
5 (bases 1 to 737)
5 (bases 1 to 737)
6 (bases 1 to 737)
7 (biret Submission )
8 (bur, Crance Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Blochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1046 CATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGAC 1103
/strain-"Ml"
/db_xref-"taxon:5022"
/clone="inan123"
/clone=lib="V8 mycelial library"
/note="Library prepared from mycelium grown in 10%
Campbell's V8 juice."
178 c 157 g 111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         866 ATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTG
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                    Length 562;
                                                                                                                                                                                                                                                       11.8%; Score 176.4; DB 12; Length
larity 63.9%; Pred. No. 1.6e-44;
Conservative 0; Mismatches 151; Indels
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BG278355
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                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                 AW180683 573 bp mRNA linear EST 17-NOV-1999
MgA0831f MgA Library Mycosphaerella graminicola cDNA clone MgA0831
S similar to catalase-peroxidase, mRNA sequence.
                                                                                                                                                                     GGAACATACAGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAA 911
                                                                                                                                                                                                                        CCACTGAACTCCTGGCCGGATAACGTAAGCCTGGATAAARCGCGCCGTCTGCTGTGGCCTT 129
                                                                                                                                                                                                                                                                                                       130 ATCAAGAAAAATACGGACAAAAATCTCCTGGGCCGACCTGTTTATCCTCGCGGGTAAC 189
                                                                                                                                                                                                                                                                                                                                                                                                             250 TGGGAACCGGATCTTGACGTGAACTGGGGTGATGAAAAACCTGGCTGAMCCACCGCGAC 309
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Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
                                                                                                                                              Gaps
                                                                                                                                             7:
                                                                                                                     Length 737;
                                                                              others
                                                                                                                   Score 171.8; DB 17; Length
Pred. No. 5.7e-43;
6; Mismatches 253; Indels
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 gambiae"
                                                                              ų
                                                                              127
          /strain="PEST"
/db_xref="taxon:7165"
/clone="108M05"
/clone=11b="NotreDame1"
/note="end : SP6"
/organism="Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1452 TATACCATCACCAGTGGCCTGGA 1474
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                                                                                                                 tch 11.5%;
al Similarity 57.3%;
357; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 CTGGTGGCCAAATGAGCTGAAACACCAAAATCCTGCGCCAGCACCACGGTGCTACCGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         812 ITATGGTCCTTTCTTTATTCGTATGCCTTGGCACGGTGCCGGAACATACAGGACATATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632 CTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATTACACAGCCCTGAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A group of expressed cDNA sequences from the wheat fungal leaf blotch pathogen, Mycosphaerella graminicola (Septoria tritici) Fungal Genet. Biol. 29 (2), 118-133 (2000) Contact: Hargreaves JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Corganism="Mycosphaerella graminicola"
/organism="Strin"
/strain="Strin"
/db.zref="taxon:54734"
/clone="MgA0831"
/clone="Mg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1052 ATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTCGGA 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 161; DB 10;
Pred. No. 1.4e-39;
0; Mismatches 187;
                                                                                                                                                                                                                        Cell Biology Department
IACR-Long Ashton Research Station
Long Ashton, Bristol, BS41 9AF, UK
Tel: +44(0)1275 392181
Fax: +44(0)1275 394281
Email: john.hargreeves@bbsrc.ac.uk
Insert Length: 2300 Std Error: 0.00
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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60.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.8
Best Local Similarity 60.1
Matches 283; Conservative
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E (bases 1 to 546)

S Freimoser, F.M., Screen, S., Baga, S., Hu, G. and St. Leger, R.J.

EST analysis of genes expressed by two different insect pathogenic fund; during optimized secretion of proteins

Contact: Freimoser F. M.

Department of Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA

Tel: 301 405 16 13

Fax: 301 314 92 90

Email: ff34@umail.umd.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1021 TGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGGATTTGCTGGCGGAA 1080
                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Metarhizium anisopliae sf. acridum ARSEF 324"
/note="Vector: Unizap; Metarhizium anisopliae sf. acridum
was grwon on insect cuticle and chitin for 24 hours. A
cDNA library was constructed in the unidirectional Lambda
vector Unizap."
169 c 149 g 103 t 13 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGCCGCCACGCAGATGGGACTTATTTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAG 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGGCCATGGATGATG 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GCAACGATGTCCGTTACAACGACAACAAGGACGTCAAGAAGCGTGATCTCGAGTCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 TGGCCGCCTCCCACATGGGTCTCATTATGTCAACCCCGAGGGTCCCGATGGAAACCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 AGGAGACTGTGGCCCTNATTGCTGGAGGCCACACCTTNGGCAAGACTCACGGTGCCCNGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1357 CTCCTGAAAATGTATTGGCGCAGGG---CCTGATGGTGCACCTGTGGAGGAGCAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 CCTTGNCACCAAAGGTTGGCCAAGNGAGCCCCCATTGANCAGCAGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081 GAGAAGATGACTGGGAGTCGGACCTGGTATACTGGGGGCCTGACAACAAGCC-----
                             Sordariomycetes;
                                             Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
                                                                                                                                                                                                                                                                                                                                                     /organism="Metarhizium anisopliae var. acridum"
/strain="ARSEF 324"
/db_xref="taxon:92637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%; Score 154.6; DB 14; Length ilarity 60.2%; Pred. No. 1.5e-37; Conservative 0; Mismatches 169; Indels
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                             Ascomycota; Pezizomycotina;
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       Metarhizium anisopliae var. acridum
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                           Eukaryota; Fungi;
                                                               Metarhizium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
297; Conserv
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Best Local Si
Matches 297;
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BH403595/c
       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                   AUTHORS
TITLE
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COMMENT
                                                                                   REFERENCE
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                                                                                                             Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Mary Anne Nelson, Department of Biology, University of
New Mexico, Albuquerque, NM 87131 (e-mail address manelson@unm.edu)
regarding clone availability
Seq primer: M13 Universal Reverse Primer
High quality sequence stop: 10cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 Wetarhizium anisopliae sf. acridum ARSEF 324 Metarhizium anisopliae sf. acridum ARSEF 324 Metarhizium anisopliae var. acridum cDNA, mRNA sequence.
BQ142683.1 GI:20279742
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Neurospora crassa"
/strain="wild type"
/db.xref="taxon:5141"
/clone="a3903np"
/clone_lib="Neurospora crassa sexual cDNA library, Uni-zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   983 ATACGGCTCCAGTATȚTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGA 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1043 ATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGAAGATGACTGGGAGTCGGA 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TGTCACGGATGGCCGTGGAGGGTGGTGGTGTTTTTGCTCCTCTCAACAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   863 GACATATGATGGCCGGGGGGGCGCCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        923 CTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAA 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            803 TTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 159.4; DB 12; Length 465; Pred. No. 4e-39; 0; Mismatches 96; Indels 3;
Sordariales; Sordariaceae; Neurospora.

(bases 1 to 465)

Kupfer,D., Lai,H., Nelson,M. and Roe,B.
ESTS from a Neurospora crassa Sexual cDNA Library Unpublished (2001)
Other_ESTS: a3903np.fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1103 CCTG---GTATACTGGGGGCCTGACAACA 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST.
Metarhizium anisopliae var. acridum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 CGAGTCTGTATACTGGGGTGCTGAGACCA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%;
69.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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us-09-674-277-1.rst

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AW180185 S71 bp mRNA linear EST 17-NOV-1999 MGA0268f MGA Library Mycosphaerella graminicola cDNA clone MGA02685' similar to PEROXIDASE/CATALASE, mRNA sequence.
        ---GTAGGAGCTGAGCCTGAATTGAAGCTCAGGGATTAGGTTGGGCAAGT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     871 ATGCCCGGGGAGGCGCCCAGTGGTCGTCAGCAACGTTTTGAACCGCTGAACAGCTGGCCGG 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 ATTGGCAAGCAGTGGACTACCCAGCGGATTCAAGAAGGTTGGATTACAATGGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1428 AAATGTGGTACAGGAAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keon, J. P. R., Balley, A. M. and Hargreaves, J. A.
A group of expressed cDNA sequences from the wheat fungal leaf
blotch pathogen, Mycosphaerella graminicola (Septoria tritici)
20374020
20374020
Contact: Hargreaves JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 CTGGTGGCCAAATGAGCTGAACACCAAGATCCTGCGCCAGCACCGCTGCTACCGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         692 CTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGC-TGGATATGGAGGCTCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="strit"
/db_xref="taxon:54734"
/clone="mgA0268"
/clone_lib="mgA Library"
/clone_lib="mgA Library"
/note="Vector: psPoRT1; Library constructed from utilizing ammonium ions as a source of nitrogen"
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Pred. No. 5.2e-31;
0; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mycosphaerella graminicola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell Biology Department
IACR-Long Ashton Research Station
Long Ashton, Bristol, BS41 9AF, UK
Tel: +44(0)1275 392181
Fax: +44(0)1275 394281
Email: john, hargreaves@bbsrc.ac.uk
Insert Length: 2500 Std Error: 0.00
Seq priner: M13 reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Mycosphaerella graminicola.
Mycosphaerella graminicola
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AW180185.1 GI:6447380
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Matches 268; Conservative
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AG-ND-127D17.TF ND-TAM Anopheles gambiae genomic clone AG-ND-127D17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        670
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                                                                                                                                                                                                                                      Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&W University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is from an A. gambiae BAC library (ND-TAM) provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  669 CCCGTACAGATGTATGGAAAGCCGATAAAGATGTATACTTGGGAAGATGAGAAAACCTGG
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                                                                                                                                                                                                                                 Shetty, J., Malek, J., Roo, H., Collins, F., Gardner, M. and Loftus Direct Submission of BAC-end sequences from Anopheles gambiae (Dapublished (2001) Other_GSSS: AG-ND-127D17.TR
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                                                                                                                            Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea;
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Pred. No. 8.2e-37;
0; Mismatches 169; Indels
                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:7165"
/clone="AG-ND-127D17"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"

    786
    70rganism="Anopheles gambiae"
/strain="PEST"

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                                                                                                                                                                                                                                                                                                                       Contact: Brendan J Loftus
                                                                                                         African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
                                                               BH403595.1 GI:17349811
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                                                                                                                                                                                          Anopheles.
1 (bases 1 to 786)
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Class: BAC ends.
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Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person
Sest nr hit (Nov. 11, 2001) gblAG60688.1|AF317697_1 (AF317697)
KatA [Burkholderia cepacia] 187 9e-47
                                                                                                                                                                                                                                                                                                                                                                                                BM865076 474 bp mRNA linear EST 07-MAR-2002 mgap008xD18f.b Magnaporthe grisea Ap Uni-Zap XR Library Magnaporthe grisea cDNA clone mgap008xD18 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             932 TAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCCAGTCAAGAAAAAATACGGCTC 991
                                                          TGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGCCGGA 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 474)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                 444 CAACGCCAATCTCGACAAGGCTCGCCCCTGTTGTGGCCAATCAAG-CAAAATTCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnaporthe grisea.
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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/clone="mgap008xb18"
/clone_llb="Magnaporthe grisea Ap Uni-Zap XR Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
Contact: Ebbole DJ
Department of Plant Pathology & Microblology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Magnaporthe grisea"
/strain="70-15"
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BM865076.1 GI:19232758
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VERSION
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BM865076
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COMMENT
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                                                                                                                         AW180270 600 bp mRNA linear EST 17-NOV-1999 MgA0361f MgA Library Mycosphaerella graminicola cDNA clone MgA03615 similar to catalase-peroxidase, mRNA sequence.
/strain="Strit"
/da_xxef="taxon:54734"
/clone="MgA0361"
/clone="MgA0361"
/clone="MgA Library"
/clone="Yectcor: pSPORT1: Library constructed from cultures
/utilizing ammomium lons as a source of nitrogen"
                                                       ATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACGGCT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           632 CTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATTACACAGCCCTGAATCAAATCC 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               752 AAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATGGTCA 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycosphaerella.

1 (bases 1 to 600)

Keon,J.P.R., Balley,A.M. and Hargreaves,J.A.

A group of expressed cDNA sequences from the wheat fungal leaf blotch pathogen, Mycosphaerella graminicola (Septoria tritici) 20374020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 132.6; DB 10; Length 600;
Pred. No. 1.7e-30;
0; Mismatches 176; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      graminicola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Hargreaves JA
Cell Biology Department
IACR-Long Ashton Research Station
Long Ashton, Bristol, BS41 9AF, UK
Tel: +44(0)1275 392181
Fax: +44(0)1275 394281
Email: john.hargreaves@bsrc.ac.uk
Insert Length: 2000 Std Error: 0.00
Seq primer: M13 reverse.

    .600
    /organism="Mycosphaerella

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Mycosphaerella graminicola.
Mycosphaerella graminicola
                                                                                                                                                                                               1050 GGATTTAAAACGCTGGGAT 1068
                                                                                                                                                                                                                   550 GGTCTGCCCACGTTTGGTT 568
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al Similarity 59.3%;
259; Conservative (
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Best Local Similarity
Matches 259; Conserv
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AW180270
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Gaps ; 1175

210

1235

270

1295

330

1355

us-09-674-277-1.rst

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P902_07d09_R Fg02_AAFC_ECORC_Fusarium_graminearum_mycelium Gibberella zeae cDNA clone Fg02_07d09, mRNA sequence.
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/organism="Gibberella zeae"
/organism="DAOM 180378"
/db_xref="taxon:5518"
/clone="F902_07409"
/clone="F902_07409"
/tissue_type="Mycelial tissue"
/dev_stage="Assexual"
  rpm) at room temperature. Culture was harvested, blended, incollated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by phredPhrap 991019 and trimmed according to phd files and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 718)
Harris,L.J., Glassco,T., Rocheleau,H., Allard,S., Chapados,J.,
Harris,L.J., Sprott,D., and Tinker,N.J.
Singh,J.A. Sprott,D. and Tinker,N.J.
Expressed Sequence Tags from Fusarium graminearum mycelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1176 CTTGCCGCCACGCAGATGGGACTTATTTATGTCAATCCTGAAGGCCCCGGTGGAAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1056 AAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTCGGACCTGGTATACTGG
                                                                                                                                                                                                                                                                                                                   1116 GGGCCTGACAACAAGCCTCTTGCAGATAACCGGGATAAAAACGGGAAACTTCAGAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                         157 TCCGAGTCCAAGAAGGCCACAAAGATA-----TTCACACACGCGACCTGGAGAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 GTGTCAGCTGCCCACATGGGTCTGATCTACGTCAACCCAGAGGGCCCTGATGGAATCCCG
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Eastern Cereal and Ollseed Research Centre
Agriculture and Agri-food Canada
Bidg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
                                                                                                                                                                                                6.5%; Score 97; DB 14; Length 417; 59.5%; Pred. No. 3.4e-19; tive 0; Mismatches 120; Indels
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Fax: (613) 759-6566
Email: harrislj@em.agr.ca.
Location/Qualifiers
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Matches 185; Conserv
                                                                                                                                   68
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JOURNAL
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BI750328
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Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@temu.edu
Chromatogram file of this sequence is available, see contact person
Sex nr hit (Nov. 11, 2001) pir/F82584 catalase/peroxidase XF2232
[imported] - Xylella fast. . . 178 2e-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="mycellum"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI
/note="Vector: producing To Theory on XhoI side of insert.
Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM869928 417 bp mRNA linear EST 07-MAR-2002 mgns008xE12f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns008xE12 5', mRNA sequence.
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                                             691
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                                                                                                                                                                                                                                                                                                       812 TTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGTGCCGGAACATACAGGACATATGA
                                                                        CTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATTACACAGCCCTGAATCAAATCC
                                                                                                                                                                                                                                                                                                                                                                                           872 TGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordarlomycetes;
Sordarlomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 417)
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/clone="mgns008xE12"
/clone_lib="Magnaporthe grisea NS Uni-Zap XR Library"
/sex="Mat1-2 hermaphrodite"
  136; Indels

    417
    organism="Magnaporthe grisea"

  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 932 TAACGTTAATCTGGATAAAGCC 953
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PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgns008 row: E c
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Magnaporthe grisea
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  Conservative
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BM869928
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948 AAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGA 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGGACCTGGTATACTGGGGGCCTGACAAC 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AAAGCTAGGCGGCTGATTTGGCCCATCAAGCAAAGTATGGCAACAAGATCTCATGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1008 GACCIGAIGGICCIGACIGGIAAIGIIGCCCIIGAAICCAIGGGAIIITAAAACGCIGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 278)
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Peterson Bldy, MS2132, College Station, Tx 77843-2132,
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                       Score 82.8; DB 14; Length 291;
Pred. No. 9.5e-15;
0; Mismatches 67; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                               /organism="Magnaporthe grisea"
/strain="Guyl1"
                                                                                       /db_xref-"taxon:148305"
          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Data: mgcm004 row: M Seq primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.6%;
Best Local Similarity 64.7%;
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: T3 primer
BACKWARD: T7 prime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1128 AAGCCTCTTG 1137
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/lab_host="E. coli (Sure cells)"
/note="Vector: Bluescript SK+/Xhol-EcoRI; Site_1: EcoRI;
Site_2: XhoI; Mycellal tissue was collected from WB agar
plates after a growth period of 6-7 days at 25 C with 14
hrs (FL/UV) day ligth exposure. Mycella was ground in
liquid nitrogen prior it's storage at -80 C until RNA
extraction. Directional cloning with 5' end of cDNA cloned
into EcoRI site of pBluescript and 3' end of cDNA cloned
into XhoI site of pBluescript (Stratagene, La Jolla, CA)."

a 250 C 185 g 116 t 4 others
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Chromatogram file of this sequence is available, see contact person
Seet nr hit (Nov. 11, 2001) dbj|BAB03310.1| (AB011415) catalase
[Sphingomonas sp.] 122 le-27
PCR PRimers
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Magnaporthe
                                                                                                                                                                                                                                                                                                                                               242
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                                                                                                                                                                                                                                                                                                                                                                                                     1213 CTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                              301 TCGCCAAGACCCACGGAGCTGGCTCAACCGACCA---CGTCGGCCCCCGAGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Magnaporthe grisea.
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                       Gaps
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Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132,
Tel: 979 845 4831
                                                                                                                                                                                                                                                Length 718;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1453 ATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87.6; DB 13;
Pred. No. 4.8e-16;
; Mismatches 130;
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Plate: mgcs014 row: P column: 15
Seg primer: T3.
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Matches 200; Conservative
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Gaps

4

Length 540; Indels 801

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540 bp mRNA linear EST 23-AUG-200:
FucusSST210 Fucus 18h embryo SST secretion library Fucus distichus
BUO38189
                                                                                                                                                                                                                                                                                                                                                                   802 ATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACA 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                         862 GGAC--ATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAA--CGTTTTGAACCGCTG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; stramenopiles; Phaeophyceae; Fucales; Fucaceae; Fucus. 1 (bases 1 to 540)
Belanger, K.D., Nyman, A.J., Sudol, M.N., Singla, S. and Quatrano, R.S. Identification of secreted polypeptides expressed in polarized Fucus distichus zygotes
Unpublished (2002)
Contact: Belanger, KD
/db_xref="taxon:3012"
/clone_lib="Fucus 18h embryo SST secretion library"
/dev_stage="18h after fertilization"
/dev_stage="18h after fertilization"
/note="vector: psuc227M130R1 SST; Site_1: EcoRI; Site_2:
XhoI; authority=Fucus distichus (L.) Powell; EcoRI/XhoI
Iragments from Fucus _ZapII random-primed Fucus DNA
library were subcloned into EcoRI/XhoI sites of
pSUC277M130RI (Jacobs et_al. 1997. Gene 198: 289)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="lBh after fertilization" //dev_stage="lBh after fertilization" //dev_stage="lBh after fertilization" //dev_stage="lBh after fertilization" //dev_stage="length: SUC2T/M130RI SUC2T/M130RI (Jecobs et al. 1997. Gene 198: 289)."

a 144 c 150 g 127 t
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/organism="Fucus distichus"
/db_xref="taxon:3012"
/clone_lib="Fucus 18h embryo SST secretion library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 AACAGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTG 967
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4.4%; Score 66; DB 14; Length 540;
Best Local Similarity 61.3%; Pred. No. 3.3e-09;
Matches 141; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                             85;
                                                                                                                                                                                                                                                      4.4%; Score 66; DB 14;
61.3%; Pred. No. 3.3e-09;
Live 0; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colgate University 13 Oak Dr., Hamilton, NY 13346, USA Tel: 315 228 7870 Fax: 315 228 7997 Email: kbelanger@mail.colgate.edu
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Best Local Similarity 61.39
Matches 141; Conservative
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Fucus distichus
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                                                                                                        /clone_injentovariation
/clone_injentovariation
/sex="Mat1-2 hermaphrodite"
/ceal_type="mycellum"
/ceal_type="mycellum"
/ceal_type="mycellum"
/note="Yector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI
; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by phredPhrap 991019 and
trimmed according to phd files and for vector seqs."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGGCATGGAT 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU038121 540 bp mRNA linear EST 23-AUG-2002
FucusSST126 Fucus 18h embryo SST secretion library Fucus distichus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1056 AAAACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTCGGACCTGGTATACTGG 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGCCGCCACGCAGATGGGACTTATTATGTCAATCCTGAAGGCCCCGGTGGAAAACCA 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fucus districtus Extramenopiles; Phaeophyceae; Fucales; Fucaceae; Fucus. Extrayota; Stramenopiles; Phaeophyceae; Fucales; Fucaceae; Fucus. 10 (bases 1 to 540).

Belanger, K.D., Wyman, A.J., Sudol, M.N., Singla, S. and Quatrano, R.S. Identification of secreted polypeptides expressed in polarized Fucus districtus zygotes
Unpublished (2002)
Contact: Belanger, KD
Department of Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 GATCCGGTTGCTGCCGCACGGGATATCCGCACTACCTTTAGCCGCATGGCCATGAACGAC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kbelanger@mail.colgate.edu
Predicted polypeptide contains an N-terminal signal sequence and
similarity to catalase protein (Bacillus subtilis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCGAGTCCAAGAAGGCCCACAAAGATA-----TTCACACACGCGACCTGGAGAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                               5.3%; Score 79.2; DB 14; Length 278; 59.0%; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 103; Indels
                           /organism="Magnaporthe grisea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 Oak Dr., Hamilton, NY 13346, USA
Tel: 315 228 7870
Fax: 315 228 7997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGAGACCGTCGCTCTGATTGCAGG 277
                                                                     /db_xref="taxon:148305"
                                                                                               /clone="mgcm004xM19"
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                                                /strain="Guyll"
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BU038121
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EST 23-AUG-2002

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AW792143 397 bp mRNA linear EST 01-MAY-2001 D01029-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei CDNA clone D01029 similar to catalase-peroxidase, mRNA sequence.
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                                                                                                                                                                                                                                                                                                              .R.P. Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis Unpublished (2000)
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Blumeria graminis f. sp. hordei
Blumeria graminis f. sp. hordei
Eukaryota; Fungl; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
1 (bases 1 to 397)
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone="D01029"
                                                                                                                                                                                                                                                                                                                                                                           Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 4766
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Best Local Similarity 59.9
Matches 112; Conservative
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Neurospora crassa
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178 TGGACTA 184
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              801
                              ATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACA 861
                                                                                                  GGAC -- ATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAA-- CGTTTTGAACCGCTG 917
                                                                                                                                                                     Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
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506 bp mRNA linear EST 01-MAY-20 D01025-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei CDNA clone D01025 similar to catalase-peroxidase, mRNA sequence.
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            AGGCTCTGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGG
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Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
1 (bases 1 to 396)
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Unpublished (2000)
Contact: Rasmussen,S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
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ilarity 59.9%; Pred. No. 5e-06;
Conservative 0; Mismatches 72;
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High quality sequence stop: 396
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Fax: 45 3327 4766
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/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
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Durham, NC 27708-1000
Tel: 919 613 8159
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                                                                                                                                                                                                                                                                                                                                                              Expressed sequences from conidial, mycelial, and sexual stages Neurospora crassa
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Pred. No. 3.4e-05;
0; Mismatches 84; Indels 2
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1. 399
/organism="Neurospora crassa"
/strain="7-0083-IV A (FGSC 2489)"
/db_xref="taxon:5141"
/clone="NM1084"
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97435549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Natvig, D.O., Nelson, M.A.
Department of Biology
University of New Mexico
Ostetter Hall, Albuquerque, NM 87
Tel: 505 277 3411
Fax: 505 277 0304
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Best Local Similarity 59.2°
Matches 125; Conservative
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Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii.

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

I (bases 1 to 591)

Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Sillow, C. and Stern, D.

Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 963

L Unpublished (2001)

Contact: Charles Hauser

DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jobes "Vector: pBlueScript SK(+) Vector; Site_1: EcoRI; Site_2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="mgct002xn01f"
/clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
/dev_stage="Germinated conidia on apprressorium-inductive
surface"
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Construction and sequence analysis of an appressorium stage cDNA library in the rice blast fungus, Magnaporthe grisea Unpublished (2001)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
Rungal Genomics Laboratory
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph_dean@ncsu.edu
Seq primer: T3 primer (AATTAACCTCACTAAAGGG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      861 AGGACATATGATGGCCGGGGGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAAC
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ilarity 52.1%; Pred. No. 0.00041;
Conservative 0; Mismatches 103;
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                                                                                                                                                                                  Another "Vector: pallorary, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min, 1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NN4 (30min, 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr), Pap-P (30min, 1hr, 4hr), TAP-P (30min, 1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NN4 (30min, 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr), Pap-B (30min, 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr), Pap-B (30min, 1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NN4 (30min, 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr), TAP-P (30min, 1hr, 4hr), NO3 to NN4 (30min, 1hr, 4hr) and NN4 to NO3 (30min, 1hr, 4hr), TAP-P (4hr, 12hr, 2min, 2hr), Saltes.

The cDNA was directionally cloned into lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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                                                                                                   /strain="CC-1690" wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
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Magnaporthe grisea cDNA clone mgae0002cc01f 5', mRNA sequence.
A1068496
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Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 877).
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Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 591;
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                                                                                /organism-"Chlamydomonas reinhardtii"
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Pred. No. 0.0023;
0; Mismatches 117;
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                 Email: chauser@duke.edu.
Location/Qualifiers
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52.2%;
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Magnaporthe grisea
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Fax: 919
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Matches 131;
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AI068496
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BF251526 537 bp mRNA linear EST 15-NOV-2001 EST418787 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAA110 5' sequence, mRNA sequence.
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                                                                                                                                                                                                                                                                               /dev_stage="Germinated conidia on appressorium-inductive surface"
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/clone_lamino
/dev_stage="spherule"
/lab_host="SOLR"
                                                                                                                                                                                                                                                /clone_lib="Magnaporthe grisea Appressorium Stage cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 GACGAIGGIAGCIACGCCCCGICCTCGTGCCTGGCTTGGCACGCTAGCGGTACCTAC
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Eukaryota; Fungi; Ascomycota; Perizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioldes.
1 (bases 1 to 537)
2 (bases 1 to 537)
3 (bases 1 to 537)
6 Cardner, M. and Kirkland, T.
Generation of ESTs from Coccidioldes immitis spherule cDNA 11
Unpublished (2000)
Contact: Malcolm J. Gardner
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The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850, USA
71: 301 838 9208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 9; Length 877
Pred. No. 0.0053;
0; Mismatches 105; Indels
Email: rdean@clemson.edu
Seg primer: T3 primer (AATTAACCCTCACTAAAGGG)
High quality sequence stop: 69.
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                                                                                                                                  /organism="Magnaporthe grisea"
/strain="70-15"
                                                                                                                                                                                          /db_xref="taxon:148305"
/clone="mgae0002cG01f"
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/clone="CIAAI10"
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Location/Qualifiers
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Best Local Similarity 51.2%;
Matches 110; Conservative
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/ Jorganism="Chlamydomonas reinhardtii"

/ strain="CC-1690 wild type mt+ 21gr"

/ db_rref="taxon:3055"

/ clone_lib="C. reinhardtii CC-1690, Stress II (normalized

), Lambda Zap II"

/ note="Vector: pBluescript II SK-; Site_l: ECORI; Site_2:

/ Note: Tress condition II library, constructed by John

Davies and Jeffrey McDermott, combines cDRAs from CC-1690

cells grown to mid-log phase in TAP (NH4+ - containing)

and shifted to TAP - NO3- (24hrs); H2 production

conditions (0, 12hr, 24hr) see Mells et al.,(2000) Plant

Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP +

sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr);

POLYA MRNA was purified from each sample, pooled and cDNA

synthesized. The cDNA was directionally cloned into lambda
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1031023D02.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
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                                                                                                                                                                                                                                                                 110 AAGGAGGACTTCCAGAAGGTTTATGATGAAATTGCAAGACTTCTTGTAGAAGGACGAT 169
                                                                                                                                                                                                                                                                                                                                                       170 TATGATGATGAAGCTACGGACCTGTCCTTGTTCGTCTCGCCTGGCACGCCAGTGGTACC 229
                                                                                                                                                                                                                                                                                                                                                                                                    858 TACAGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                230 TACGATAAGGAAACTGGGACTGGAGGAAGCAATGGCGCTACCATGCGCTTCGCCCCATAG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            918 AACAGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAG 977
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                                                                                                                                                                                                                                                                                                               GCGGATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACA 857
/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1"
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                                                                                                                                                                                                                       ATGGAGGCTCTGAAAAAAAAATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCT
                                                                                                                                Score 45.8; DB 12; Length 537;
Pred. No. 0.0095;
0; Mismatches 137; Indels 0
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Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
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Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
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BI718013.1 GI:15693708
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Durham, NC 27708-1000
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18 Similarity 48.38;
128; Conservative
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AW/89645 EST 01-MAY-2001 CO1253-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei CDNA clone C01253 similar to catalase, mRNA sequence.
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Blumeria graminis f. sp. hordei
Blumeria graminis f. sp. hordei
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphaceae; Blumeria.
1 (bases 1 to 335)
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
                                                                                                                                                                                                                                                                                     860
                                                                                                                                                                                                                                                                                                                    861 AGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAAC 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                              525 GCCAAGAAGGACGGCGGCAGCAACAGGGCCACCATGCGCTNTGCTCCCGAGTGC
                                                                                                                                                                                                                                                                                  801 GATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1008 GACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were exclsed from lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806.
                                                                                                                                                                                                                                              Gaps
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/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone="C01253"
/clone="c01253"
/clone="condia"
/lab_host="Hordeum vulgare"
/d a 70 c 78 g 91 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 335;
                                                                                                                                                                                                   Length 660;
                                                                                                                                  1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                               Score 44.8; DB 13;
Pred. No. 0.023;
0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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Pred. No. 0.031;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 335
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                                                                                                                                                                                               Query Match 3.0%;
Best Local Similarity 53.1%;
Matches 94; Conservative (
                                                                                                                                       231c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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LEADLITE SUBMISSION

SUBMITTED (102-JUN-1999) Genoscope . Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www. genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Prosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillers for hybridization from the BACPAC Resource Center can be incention/Qualifiers

Liceation/Qualifiers
                                                         CNS001N6 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR04B08 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ539839 694 bp mRNA linear EST 12-JUN-2002 PTAM0150 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum tricornutum cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536 TATGATAAAAAAACTCTTCCTGTTCTGATTCTTCTGGCGCTATCGGGGAGCTTTTCTAC 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               656 AACTCCTCTGAGATTACACAGCCCTGAATCAAATCCCTGGGGGGGCTGATTTGATTATGC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    596 CGCTGTAGCCGCTGATAAAAAGAGACTCCAAAATTTCTACTATCCAGAAACACTGGATTT
                                                                                                                                                                                                                                     Drosophila melanogaster.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 1101)

Genoscope.

Direct Submission
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; Pred. No. 0.79;
43; Mismatches 99; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYWAAAWTTKGMATTACWGCKRAKGWAAAGWATKKAAAA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-*Drosophila melanogaster"
/db_xref="taxon:727"
/clone="BACR04B08"
/clone=1ib="RRCI-98"
/note="end: TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 t
                                                                                                                  fly), genomic survey sequence. AL061217
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BQ539839.1 GI:21395409
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BQ539839
                                                                                                                                                              ACCESSION
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/organism="Chlamydomonas reinhardtii"
/strain="Cc-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="Cc. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_l: EcoRi; Site_2:
Xhol; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4 - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hrs); H2 production
conditions (0, 12hr, 24hr); TAP + H3C2 (1, 12, 24 hr); TAP +
Sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr)
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized 'The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5) and XhoRI (3)
sites: pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with Exasist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
Chlamydomonadaceae; Chlamydomonas.
I (bases 1 to 640)
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Onicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
Onpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
                                                                                                                                                      BI717417
1031019G07.y1 C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
BI717417
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106 t
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                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: chauser@duke.edu.
                                                                                                                                                                                                                                                           BI717417.1 GI:15693112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Best Local Similarity 52.3v
Rest Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        945 GATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1005 GGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTG 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 rcgaacggreeccrarecerrrraccccccaagccggareggecccaacgcccggacrc 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 GCCGACCTCTACACCTACGCTGGTCGTCGCGGTGGAAGAAGCCGGAGGCCCTATCATT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 543)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Mussell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Dipublished (1999)
Other_GSSs: RPCI-24-316M7.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825 TITATICGIAIGGCIIGGCACGGIGCCGGAACAIACAGGACAIAIGAIGGCCGGGGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:2850" /clone_llb="Phaeodactylum tricornutum Uni-Zap XR" /cell_line="CCMP632"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 14; Length 694;
Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Phaeodactylum tricornutum"
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Location/Qualifiers
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                       Phaeodactylum tricornutum,
                                                                                                                                                                                                                                                                                                          Email: chris@alpha.szn.it
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Similarity 49.3%;
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/cell_type="Spleen/Brain" /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
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                                                                                                                                                         Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejongémail.cho.org). Clones may be purchased from BACPAC Resources (http://www.clori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html blate: 316 row: M column: 7 Seq primer: Sec order.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 TICTACCGCTGTAGCCGCTGATAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650 GGATTTAACTCCTCTGAGATTACACAGCCCTGAATCAAATCCCTGGGGGGGCTGATTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 AGGTCAAATATTTTGTTTTTCTGCTCATTACCACAGTCTTGGTTACATTTTCTGAA
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism~"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/63"
/db_xref="taxon:10090"
/clone="RPCI-24-316M7"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..543
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University of Delaware
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                                                                                                                                      Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%;
Best Local Similarity 50.8%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
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Submitted (23-70L-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@enoscope.cns.fr-Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNSO18FX 803 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN13P04 of DrosbAC library from Drosophila melanogaster (fruit
                            /clone_lib="AT Drosophila melanogaster adult testes pOTB7"
                                                                                                                                        /note="Organ: ADULT festes; Vector: poTB7; Site_1: ECORN Site_2: Khol; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into poTB7. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                         1329 ACATTIGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      688 GCTGCAGCTGCAGAAGAACATCAACGAGCTAAAAGCAAGAATCGTTGAATTGGAGTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; brosophila.
1 (bases 1 to 803)
                                                                      /dev_stage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
                                                                                                                                                                                                                                                                                                                                                  Score 39.4; DB 12; Length 775; Pred. No. 1.3;
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /plasmid-"pBeloBAC11"
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                                                   /sex="male"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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htt genomic AE003655: arm:2L [17213419,17469171]
estimated-cyto:36C1-36C8: 04/07/2001
Plate: AT.25 row: G column: 6
High quality sequence stop: 697.
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On Dec 6, 2000 this sequence version replaced gi:11577451.
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                                                                                                                                                                                                                                                                                                                                                                                             Length 661;
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                                                                                                                                                                                /clone="pglln.pk010.g23"
/clone_lib="Normalized Liver Library"
/sex="Male and Female"
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/db_xref="taxon:7227"
                                                                      Email: joan@UDel.Edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       79;
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One Cyclotron Rd, Berkeley, CA 94720, USA
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                                                        Score 39.6; DB
Pred. No. 1;
0; Mismatches
                                                                                                                                                                                                                                                  /tissue_type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pcMvSpORT 6"
1 208 c 184 g 119 t
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    .661
    /organism="Gallus gallus"

                                                                                                                                                             /db_xref="taxon:9031"
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Celniker, S. and Rubin, G.M.
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52.48;
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 52.4 tes 87; Conservative
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Fax: 510 486 6798
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tracheophyta;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1095)
                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="TO10000DH3"
/db_xref="taxon:3712"
/clone="BOMBA22"
/clone="lbb-"BO_2_3_KB"
/clone=lib-"BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
152 c 99 g 298 t
                                                        Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                         1 (bases 1 to 829)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
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                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                              Tom
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Pred. No. 3.4;
); Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Brassica oleracea"
                                                                                                                                                                                                                                                                      Tel: 301-838-3523
Fax: 301-838-0508
Email: cdtown@tigr.org
DNA is from a doubled haploid pu
Seq primer: TF
Class: sheared ends.
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Unpublished (2001)
Other_GSSs: BOWBA22TR
Contact: Chris Town
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                                       Brassica oleracea
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Bukaryota: Mycetcoza; Dictyosteliida; Dictyostelium.

1 (Bases I to 717)

Worlo, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Marda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. Unpublished (1998)

Contact: Hideko Urushihara

Unstitute of Biological Sciences

University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                              C90436 177 bp mRNA linear EST 20-APR-1998 C90436 Dictyostellum discoideum SS (H.Urushihara) Dictyostellum discoideum cDNA clone SS1494, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364
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                                                                                                          568 TTCTGGCGCTATCGGGGAGCTTTTCTACCGCTGTAGCCGCTGATAAAAAAGAGACTCAAA 627
                                                                                                                                                                                 628 ATTICTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATTACACAGCCCTGAATCAA 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="SSI494"
/clone_lib="Dictyostellum discoideum SS (H.Urushihara)"
/dev_stage="slug"
| 115 c 92 g 228 t
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Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.2; DB 14;
Pred. No. 3.1;
0; Mismatches 48;
 92;
 91; Mismatches
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/db_xref="taxon:44689"
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1 Similarity 58.3%;
67; Conservative
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C90436.1 GI:3060056
   Conservative
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43;
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Email: est@watson.wustl.edu
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Best Local Similarity 50.9
Matches 143; Conservative
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              TITLE
JOURNAL
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutcyo Osocgawa and Aaron Mammoser in Fiteter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Encophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW707196 599 bp mRNA linear EST 03-DEC-2001 sk22a06.yl Gin-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-2891 5' similar to TR:Q39780 Q39780 ASCORBATE PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 THTHTHNSSSNNNNNNSSSANNAANNNNSSSNNNTSNNNNNNNNNANAAANTNNNNNTNNT 500
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 GACAICCACAAAGAAGGGAAIATICAGGICIGCGCAGCACICAACGGCAICGICAGTIGC 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="BACR22A01"
/clone_lib="RPCI-98"
/note="end : T7"
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AW707196
AW707196.1 GI:7591464
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681 TSSSNSTINTAVVAA 695
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Best Local S:
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AW707196
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KEYWORDS
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REFERENCE AUTHORS

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/tissue_inpe="roots of 'Supernod' plants"
//tissue_inpe="roots of 'Supernod' plants"
//lab_host="DH10B"
//lab_host="DH10B"
//lab_host="DH10B"
//note="Vector: BBluescript II XR; Site_1: ECORI; Site_2: XhoI; The manA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizoblum japonicus, strain USDA110 priot to harvest. Stratagene's cDNA synthesis Rit (catalog number 200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dTPP, hence the ligated CDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A.C. or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAACATAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the CDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EconI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by their hemimethylated status. The CDNA constructs were size-fractionated with a 500bp cutoff, using GibcobRL Life Technologies' CDNA size Fractionation Stratagene's spluescript II SR(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white end blue colonies appear to contain recombinant plasmids with cDNA inserts. hased on size of company.
                                                                                                                                                                                                                                                                  This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or context via email: ccu@resgen.com
Insert Length: 1196 5td Error: 0.00
High quality sequence stop: 422.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              999 TCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAA 1058
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fat: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-2891"
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Pred. No. 3.
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A1980795 652 bp mRNA linear EST 07-MAY-2001 pat.pk0033.f8.f chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0033.f8.f 5' similar to amyloid precursor protein, mRNA
                                                                                                                                                                         999 TCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAA 1058
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1 (bases 1 to 652)
Tirunagaru, V.G., Sofer, L., Cul, J. and Burnside, J. An expressed sequence tag database of T-cell-enriched activated Genomics 56 (2), 144-151 (2000)
20318616
Contact: Joan Burnside
                                           210 GGAGGCCCTAATGGTTCTATCAGAACAGACTAGAGTTGAATCAC---GCAGCAAACAAG
    GGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGCCGGATAACGTT
                                                                                       939 AATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAAATACGGCTCCAGTATT
                                                                                                                                  GGACTGGAAACAGCACTTGCCTTCTGTGAGGAAGTGAAGGCCAAACA---TCCAAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pat.pk0033.f8.f"
/clone_lib="chicken activated T cell cDNA"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splenic T cell"
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                                                                                                                                                                                                                                                                 1059 ACGCTGGGATTTGCTGGCGGAAGAAGATGACTGGGAGTC 1099
                                                                                                                                                                                                                                                                                          joan@UDel.Edu, www.chickest.udel.edu
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University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
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/lab_host="E.coli TOP10 F'"
/note="Vector: pcDNA3"
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Best Local Similarity 49.7%;
Matches 96; Conservative (
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AI980795.1
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AI980795
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VERSION
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Khoi; This CDNA library was constructed from mRNA isolated
from etiolated hypocotyl issue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dr) primer with a Xhoi restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by digestion with ECORI and Xhoi The CDNA
fragments were directionally cloned into the ECORI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This close is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1062 Std Error: 0.00
High quality sequence stop: 426.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker, R., Kelin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Hitter, E., Kohn, S., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                  BES56340 61-20145 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1045-1868 5' similar to TR:Q39780 Q39780 ASCORBATE PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Hypocoty1, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papllionoideae; Phaseoleae;
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Gibco BRL). This library was constructed by Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .635
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENONE SYSTEMS CLONE ID: Gm-c1045-1868"
/clone_lib="Gm-c1045"
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1059 ACGCTGGGATTTGCTGGCGGAAGAGATGACTGGGAGTC 1099
                      DB 10;
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Pred. No. 3.8;
0; Mismatches 132;
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                                                                                                                                                                                                                     mRNA sequence.
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VERSION KEYWORDS SOURCE

ACCESSION

RESULT 44 AW180016

LOCUS

AUTHORS TITLE

REFERENCE

JOURNAL MEDLINE COMMENT

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587 bp mRNA linear EST 26-JUN-2002 sap65a03.yl Gm-C1087 Glycine max CDNA clone SOYBEAN CLONE ID:
Gm-C1087-5382 5' similar to TR:Q9SXL5 Q9SXL5 CHLOROPLAST ASCORBATE PEROXIDASE PRECURSOR;, mRNA sequence.
BQ611766
BQ611766.1 GI:21601435
EST.
Bumphray, S.J., Huckle, E. and Hunt, S.E.
Direct Submission
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail contact: hunquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 22018. 22018 is part of the Danlokey Pilot BAC Library created by R. Plasterk and N.V. Keygene.
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                            Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
1. .630
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 129;
                                                                                                                                                                                                                                                         /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="Drkey-2018"
/tissue_type="Testis"
/note="vector pindigobac-536"
a 59 c 82 g 230 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37.6;
Pred. No. 4.
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Best Local Similarity 47.1%;
Matches 115; Conservative
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AW180016 GI:6447211 EST.
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Scrinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 630)
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
Mycosphaerella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keon, J.P.R., Balley, A.M. and Hargreaves, J.A. A group of expressed cDNA sequences from the wheat fungal leaf blotch pathogen, Mycosphaerella graminicola (Septoria tritici) Fungal Genet. Blol. 29 (2), 118-133 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37.6; DB 10; Length 627; Pred. No. 4.4; O; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mycosphaerella graminicola"
/stralin="Strii"
/db_xref="taxon:54734"
/clone="MgA0072"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Hargreaves JA
Cell Biology Department
IACR-Long Ashton Research Station
Long Ashton, Bristol, BS41 9AF, UK
Tel: +44(0)1275 392181
Fax: +44(0)1275 394281
Email: john.hargreaves@bbsrc.ac.uk
Insert Length: 2500 Std Error: 0.00
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Mycosphaerella graminicola
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                                                        1390 GTGCACCTGTGGA 1402
                                                                                  | || || || || GCCCAGCTGCAGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Conservative
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Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio rerio
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              122
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ORIGIN
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FEATURES

ACCESSION

VERSION KEYWORDS

REFERENCE

RESULT 45

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Gaps

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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
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Best Local S
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TITLE
JOURNAL
                                                    JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com & Seq primer: -40mP from Gibco
High quality sequence stop: 431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4/0 DP mRNA linear EST 22-JAN-2001
hu62a05.xl NCI_CGAP_Brn41 Homo sapiens CDNA clone IMAGE:3174440 3',
mRNA sequence.
BF940954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            981 AAATACGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTT 1040
                                                                                                                                                                                                                                        /tissue_type="Roots"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI: "He mRNA was prepared using polyatract mRNA system
from PROMEGA. The CDNA was prepared using the STRATAGENE
Att. Complementary DNA was synthesized from mRNA using a
primer consisting of a poly(dT) sequence with a XhoI
restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATAC 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   861 AGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAAC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 GAGCATGCCAACGCCGGCCTCCAGGTCGCTCGCGGACCTTCAGGAACCCATCAAGAAG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 CAGT---TCCCTTGGATCAGCTATGCAGACCTGTGNACCTGGCTGCTGCTAGCAGTT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 GACGATGGCAGCTATGGCCTGTGTGAGGCTGGCCTGGCACGCCAGCGGCACCTAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 476)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921 AGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1041 GAATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAGATGAC 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 GAAGCGATGGGAGGTCCTGAGATTGCTTGGAGGCCCGGCCGCAAAGACCAC 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.2; DB 14; Length
Pred. No. 5.7;
0; Mismatches 149; Indels
                                                                                                                                                    1. 587

/dorganism="Glycine max"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1087-5382"

/clone_lib="Gm-c1087"
                                                                                                                                      Location/Qualifiers
Fax: 314 286 1810
Email: est@watson.wustl.edu
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ilarity 47.8%;
Conservative
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC15B10 Pine TriplEx pollen cone library Pinus taeda cDNA clone PC15B10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1211 TCCTGAAGGCCCCGGTGGAAAACCAGATCCTCGGCTTCCGCGAAAGATATCAGGGAAGC 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1271 TITITCACGIATGCCCATGCATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGCCATAC 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. I, (bases I to 520)
Whetten, R.W., Killaw,C.S., Retzel,E. and Sederoff,R.R.
The Pine Gene Discovery Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 CITIGETICCIACAGGCIGGAIGGIAICCCTGGAAGCCITGTAGGCCCACAGCCCTG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1331 ATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAA----TGTATTGGCGCAGGGCCTG
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov
Email: cgapbs-rémail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 TGCTCAGGCCCCCATAGGATAAACAGATTGGTGGGGCCCTGGAGATAGAAGGAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 TATATGTGGTACTGGGGAGGAAGAAGAAGAAGTNANCCNNTTAGAGCCACTTTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 GTAGGCTCCTGGGAAAGAGAAGGACAGCG 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1
Pred. No. 5.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                     infoelmage llnl.gov
Seg primer: -400P from Gibco
High quality sequence stop: 475.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW981658.1 GI:8173224
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COMMENT

FEATURES

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/db_xref="taxon:6279"
/clone_llb="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
/tissue_type="Whole parasite"
/dev_stage="microfilaria (L1)"
/dev_stage="microfilaria (L1)"
/note="Vector: pBAce3.6; Site_1: BamH I; Brugia malayi
genomic DNA was partially cleaved with Sauah I and size
fractionated 7,392 clones were generated with mean insert
size -48 kbp. The library was constructed by Claire
Whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genome survey sequence T7 end of BAC #BACR11006 of RPCI-98 library from Drosophila melanogaster (fruit AL058090
                                                                                                                                                                                                                                                                                          Sequenced from the Brugia malayl BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, UK.
Seq primer: I7 (TAATACGACTCACTAIAGGG)
class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617 AGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATTACACAG 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 ACAGACTAAATTTTTGCAAACCATAAACTTGAAATAATAAAATGACAAAATCACAGCA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 CCCTGAATCCAAATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGA 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 CTATTAGATCATACCTTCAGATCATTACTTTGAGAAATCAACCACTTGTGAATAAATTCC 205
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefêgenoscope.cns.fr
                                          Unpublished (2000)
Context: Blaxter ML
Contitute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         737 TATGGAGGCTCTGAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATT 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
2.5%; Score 37; DB 17; Length 637;
Best Local Similarity 50.9%; Pred. No. 6.9;
Matches 88; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Brugia malayi"
                                                                                                                                                                                                           Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="TRS"
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/organism="kinus taeda"
/db_xref="taxon:3352"
/clone="pc15810"
/clone="lb="pine TriplEx pollen cone library"
/clone=lb="pine TriplEx pollen cone library"
/dab_host="E. col! BM25.8"
/lab_host="col! BM25.8"
/lab_host="col! BM25.8"
/note="organ: pollen cone; Vector: Lambda TriplEx; Site_1: Sfil (A); Site_2: Sfil (B); Immature pollen cones were collected in the early spring, frozen and used for mkNa isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in prinplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."
sequenced from the 5' end."
9 others
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Brugia malayi
Brugia malayi
Brugia, Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Buchocercidae; Brugia.

1 (bases 1 to 637)
Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster,J., Guiliano,D., Slatko,B. and Blaxter,M.
Genome survey sequences from the human parasitic nematode Brugia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               991 CCAGTATITCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGG 1050
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BMBAC330H08T7_PSU Brugia malayi Genomic Bac Library 3 Brugia malayi
Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
NC, 27695-8008
NC, 27695-8008
Fax: 919-515-7801
Email: rosswheteunity.ncsu.edu
Seq primer: 5' lambda TriplEx2 Sequencing Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         811 ATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACATATG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931 ATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCCAGTCAAGAAAAATACGGCT 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 CGAAGACGGGTGGGGCAAATGGTTCCATTAGAAACGAGGAGGAACTCAATCACAGTGCAA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 GAGGICCCACAATIGAGITIGICCCIGGICGIAAGGATICACIGGGATCAACACGAGAAN 404
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48.9%; Pred. No. 6.1;
tive 0; Mismatches 157; Indels
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BH762769
BH762769.1 GI:19558318
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BH762769/c
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
                                                                                                                                          melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 CATCCACAAAGAAGGGAATATTCAGGTCTGCGCAGCACTCAACGGCATCGTCAGTTGCGG 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 TITCAGGATACCCTTCGTCATCAACACGTACAAACCAGAAGACCAGCTTTTTGTTTCTGA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 CTTGGAACCCCTTAGTATTTTTGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGT 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCATCAATAAAGTTGACTTTTGTATACAACATGCGAATTTCCCTTAATCCGGAGCTATT 533
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                                                           The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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    1024
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

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Job time : 1591.88 secs
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The present sequence is specific to enterohemorrhagic Escherichia coli (EHEC). The sequence is 99.9% homologous to the katp gene of E. coli 0157:H7 (nucleotides 407-1489 of the present sequence), and 95.8% homologous with IS91 of E. coli (nucleotides 1-406 of the present sequence). The present sequence is of plasmid origin. Fragments of the present sequence are used, as probes and primars, for detection of E. coli 0157:H7 and other enterohemorrhagic E. coli (EHEC), in human or animal samples, foods or the environment. The fragments are also useful Enterohemorrhagic Escherichía colí; EHEC; katP gene; E. coli 0157;H7; Nucleic acid sequence specific to enterohemorrhagic Escherichia coli, New nucleic acid containing sequences specific to enterohemorrhagic Escherichia coli, particularly serotype 0157:H7, used for detecting these bacteria in food Sequence 1489 BP; 386 A; 354 C; 391 G; 358 T; 0 other; (SNFI) PASTEUR SANOFI DIAGNOSTICS. Laure FC, Thierry D; AAZ36101 standard; DNA; 1489 BP Claim 1; Fig 1; 48pp; French. 99WO-FR01000. epidemiological studies. 98FR-0005329 (first entry) WPI; 2000-013443/01 Escherichia coli. Frechon DTM, WO9955908-A2. 28-APR-1998; 27-APR-1999; 11-FEB-2000 04-NOV-1999 AAZ36101; 61 61 121 Query Match 121 181 RESULT 1 AAZ36101 NAME OF COLOR OF STREET OF 셤 ŏ 8 ò g Human breast cell Human foetal liver Probe #11883 for g Human brain expres Human cDNA clone (Fungal ZBC gene se Drosophila melanog Drosophila melanog #2092 used t foetal liver foetal liver #9031 for ge #19594 for g bone marrow Membrane-bound pro Human cDNA sequenc Human PRO1154 (UNO Yeast AOD9604-asso Pneumococcal patho Human prostate can Human differential prostate exp Human prostate exp Human prostate exp secreted pro Human colon cancer Human polynucleoti for ge for g Iron uptake ABC tr Human cDNA sequenc Hansenula polymorp Human nervous syst !uman nervous syst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is of the Microscilla furvescens catalase-53CA1 gene. Fragments of the gene can be used to identify related sequences. Catalase-53CA1 may be used to catalyse oxidation reactions such as epoxidation or hydroxylation. The enzyme can also be used to detect or
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0; Mismatches 264; Indels 6;
            GAAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGAC
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                                                                                           ATACGGCTCCAGTATTTCCTGGGGAGACCTGATGTCCTGACTGGTAATGTTGCCCTTGA 1042
                                                                                                                                                                                                                                             AGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTC 1276
                                                                                                                                                                                                                                                                                                                      1337 TAAAGCACATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACC 1396
                                                                                                                                .043 ATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAGATGACTGGGAGTC--- 1099
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                                                                                                      648 CCGAGAGCTCGAAAATCCCCTGGGAGCCGTACAAATGGGACTCATCTATGTAAACCCCGA 707
                                    407
                                                                       TTACGGTCATTATGGCCCCTTCTTTATACGCATGGCGTGGCACAGCGCCGGCACCTACCG 347
                                                                                                                                                                                                                                                        828 AAAAACCCATGGTGCTGCCGATGCGGAGAAATATGTGGGCCGAGAGCCTGCCGCCGCGGGG
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                                                                                                                                          100 GGACCTGGTATACTGGGGGCCTGACAACAACCCTCTTGCAGATAACCGGGATAAA---AA
                                                                                                                                                                                 1277 ACGTATGGCCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGAGGGCATACATTTGG
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                  GACATATGATGGCCGGGGGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAG
                                    TATCGGTGATGGCCGTGGCGGGGGCTCCCGGCTCACAGCGCCTTCGCGCCTCTCAATAG
                                                        CTGGCCGGATAACGTTAATCTGGATAAAGCCCCGTCGATTGCTGTGGCCAGTCAAGAAAAA
                                                                                                                                                                                                         Tuberculosis; katG gene; isoniazid resistance; INH;
isonicotinic acid hydrazide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                          948 CATCACCAGTGGACTAGAAGGCGCCTGGACCA 979
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GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCA 1047
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                                                                                                                                                                                 Determination of isoniazid sensitivity of Mycobacterium tuberculosis strains – by restriction length polymorphism analysis of katG gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.0%; Score 298.4; DB 19; Length 2235; 62.4%; Pred. No. 5.5e-86;
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                                                                                                                                                                                                                                                                        Claim 1; Column 9-12; 18pp; English
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Conservative
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(MAYO-) MAYO FOUNDATION
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                                       AGCAGGGACTGGGATGGAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCA 1464
      ATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAGG 1404
                                                 Areacecec---ecceeccearcreerceecceeaaceceaecrecreereeaec
                                                                                                                                                                                                                                                                                                                                                                                                                                         e to T transversion at base 1457 alters codon 463 from CGG (Arg) to CTG (Leu) leading to isoniazid resistance, and eliminates a Ncil-MspI restriction site"
                                                                                                                                                                                              Isoniazid resistance; restriction fragment length polymorphism; RFLP; katG gene; catalase; peroxidase; multiple drug resistance; isonicotinic acid hydrazide; INH; tuberculosis; antibiotic;
                                                                                                                                                                                                                                                                                                                                         "G to C transversion at base 1013 alters codon 315 from AGC (Ser) to ACC (Thr) leading to isoniazid resistance, and produces a new MspI restriction site"
                                                                                                                                                                                                                                                                                                                                                                                                    alters
                                                                                                                                                                                                                                                                                                    alters
                                                                                                                                                                                                                                                                                                "G to C transversion at base 859 alter:
codon 264 from GCG (Ala) to ACG (Thr)
leading to isoniazid resistance, and
eliminates a CfoI restriction site"
                                                                                                                                                                                                                                                                                                                                                                                                 A to G transversion at base 1079 alter
codon 337 from TAC (Tyr) to TGC (Cys)
leading to isoniazid resistance, and
eliminates a Rsal restriction site"
                                                                                                                                                                               Mycobacterium tuberculosis wild-type katG gene.
                                                                       GTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 CCGACAACGCCAGCTTGGACAAGGCGCGCCGGCTGTGCCCGGTCAAGAAGAAGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTATTGGGGCAAGGAAGCCACCTGGCTCGGCGATGAGCGGTTACAGCGGTAAGCGGGATC
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                                                                                                                                                                   This DNA sequence comprises a consensus of the Mycobacterium tuberculosis wild-type katG (catalase-peroxidase) gene. Claimed methods of rapidly identifying strains of M. tuberculosis which are resistant to the tuberculostatic drug isoniazid (INH) are based on the discovery of 4 mutations in the wild-type gene sequence that confer INH resistance and which coincidently result in the addition or deletion of restriction endonuclease sites. Primers (see AAT90401-02) are provided for the PCR amplification of the katG gene of a test strain of M. tuberculosis, and further primers (see AAT90403-06) for uses in the restriction fragment length polymorphism analysis of the amplified gene, and hence for determination the susceptibility to INH of the strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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by detecting mutation(s) in the catalase-peroxide gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%; Score 298.4; DB 18; Length 2331; 62.4%; Pred. No. 5.6e-86; ive 0; Mismatches 296; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2331 BP; 455 A; 734 C; 763 G; 379 T; 0 other;
                                                                                                                   Claim 1; Column 31-36; 38pp; English
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Matches 502; Conserv
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention realtes to a novel method of detecting Mycobacterium tuberculosis. The method comprises amplifying the DNA in the samples to generate a detectable amount of amplified DNA comprising a catalase-peroxide (katG) DNA fragment with sequence of bases 904-1523 of the M. tuberculosis strain H37kv MC katG gene sequence. The method optionally turther comprises determining if the katG DNA fragment has a serine to threonine mutation in codon 315 (S15T mutation), indicative of an isonicctinic acid hydrazide (IMR)-resistant M. tuberculosis strain. The method can be used to detect M. tuberculosis in biological fluids, especially human sputum, useful to diagnose tuberculosis. This disease is a major cause of human morbidity and mortality, and conclusive diagnosis and subsequent treatment depends on identification of the etiologic agent M. tuberculosis. INH has been used in tuberculosis treatment, but we may be a sequence of the method of the conclusive diagnosis.
                                                         953 AGATGGGCTTGGGCTGGAAGAGCTCGTATGGCACCGGAACCGGTAAGGACGCGATCACCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis. INH has been used in tuberculosis treatment, but
INH-resistant strains have emerged; the method allows such drug-resistant
strains to be identified. The present sequence represents the wild-type
896 ATGGCGCCG---GCCCGGCCGATCTGGTCGGCCCCGAACCCGAGGCTGCTCCGCTGGAGC 952
                               1405 AGCAGGACTGGGATGGAAAAATAAATGTGGTACAGGAAACGGCAAATATACCATCACCA
                                                                                                                                                                                                                                                                                                                       Catalase-peroxide; katG; isonicotinic acid hydrazide; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection of Mycobacterium tuberculosis - by amplifying katG gene and detecting specific fragment, and optionally identifying INH-resistant strains by detecting specific mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "catalase peroxide"
/note= "the start codon is not indicated"
                                                                                                                                                                                                                                                                                          M. tuberculosis catalase peroxide (katG) gene sequence
                                                                                          GTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                                            1013 GCGCCATCGAGGTCGTATGGACGA 1036
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70..2292
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/gene= "katG"
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                                                                                                                                                                                                AAX00817 standard; DNA; 2331
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P-PSDB; AAW95398.
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Sequence 2331 BP; 455 A; 734 C; 763 G; 379 T; 0 other;

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CCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGAGGGCATACATTTGGTAAAGCAC 1344
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                                                                                                                                                                                                                                                                                                                                                                                                                       GCICCAGIATITCCIGGGGAGACCIGAIGGICCIGACIGGIAAIGIIGCCCIIGAAICCA 1047
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                                                                                                                                                                         296 TGACGCGGGACATCGAGGAAGTGATGACCACCTCGCAGCCGTGGTGGCCCGCCGCCGACTACG 355
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                                                                   688 ATCCCTGGGGGCCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTC
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                                    Indels
Score 298.4; DB 2
Pred. No. 5.6e-86;
0; Mismatches 296
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 20.0%;
62.4%;
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Matches 50
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2152543 ATGGCGCCG---GCCCGGCCGATCTGGTCGGCCCCGAACCCGAGGCTGCTCCGCTGGAGC 2152487
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                                                                                            2152663 ACGCAACCCGGACCCCATGCCGCGGCGGTCGACATTCGCGGAGACGTTTCGCCGATGG
                                                                  1225 GTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTTTCACGTATGG
                                                                                                                                                                                                                                                     1285 CCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGGGGGCGCATACATTTGGTAAAGCAC
                                                                                                                                                                                                                                                                                             2152603 CCATGAACGACGTCGAAACAGCGGCGCTGATCGTCGGCGGTCACACTTTCGGTAAGACCC
                                                                                                                                                                                                                                                                                                                                             ATGGTGCAGCGTCTCCTGAAAATGTATTGGCGCAGGGCCTGATGGTGCACCTGTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, whycobacterium by determining the nuclection that complete sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 155! (Ar199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of the tuberculosis genetics, epidemiology, patient treatment and epidemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748 TGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATG
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                                                                                                                                                                                                                                                                                                                                                                                   Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37kv differ
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llarity 62.4%; Pred. No. 6.2e-84;
Conservative 0; Mismatches 296; Indels
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                   Mycobacterium tuberculosis
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                                                                                                                       688 ATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTC 747
monitoring. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                    Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2155463 TGGAGAACCCGCTGGCCGGGGGGAGGGCTGATCTACGTGAACCCGGAGGGCCGA
                                                                                                                                                                               2155403 ACGCAACCCGGACCCCATGCCGCGGTCGACATTCGCGAGACGTTTCGGCGATGG
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Pred. No. 6.2e-84;
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                                                                          Query Match 20.0%;
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Matches 502; Conservative
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The invention realtes to a novel method of detecting Mycobacterium tuberculosis. The method comprises amplifying the DNA in the samples to generate a detectable amount of amplified DNA comprising a catalase.

Generate a detectable amount of amplified DNA comprising a catalase peroxide (katg) DNA fragment with sequence of bases 904-1523 of the M. tuberculosis strain H37Rv MC katG gene sequence. The method optionally turberculosis strain H37Rv MC katG gene sequence. The method optionally threonine mutation in codon 315 (33157 mutation), indicative of an isonicotinic acid hydrazide (INH)-resistant M. tuberculosis strain. The method can be used to detect M. tuberculosis in biological fluids, especially human sputum, useful to diagnose tuberculosis. This disease is a major cause of human morbidity and mortality, and conclusive diagnosis and subsequent treatment depends on identification of the ethologic agent M. tuberculosis. INH has been used in tuberculosis treatment, but INH-resistant strains have emerged; the method allows such druy-resistant strains to be identified. The present sequence represents the M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of Mycobacterium tuberculosis - by amplifying katG gene and detecting specific fragment, and optionally identifying INH-resistant strains by detecting specific mutation
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                                                                 Catalase-peroxide; katG; mutation; isonicotinic acid hydrazide; INH; tuberculosis; diagnosis; detection; variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: this sequence is not provided in the specification; it created by modifying the katg gene sequence given in Fig 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compared to the
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M. tuberculosis catalase peroxide (katG) gene variant
                                                                                                                                                                                                                                                                                                                                                                                    "catalase peroxide variant"
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Kline BC,
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                                                                                                                          GCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTGAATCCA 1047
                                                                                                                                                             TGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAAAATGACTGGGAGTCGGACCTGG 1107
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                                                                                                                                   TCTATTGGGGCAAGGAAGCCACCTGGCTCGGCGATGAGCGTTACAGCGGTAAGCGGGATC 715
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TGACGCGGGACATCGAGGAAGTGATGACCACCTCGCAGCCGTGGTGGCCCGCCGGCGACTACG 355
                                                                                                                                                                                                                                               ATGATGGCCGGGGGGGGCGCCAGTGGTGGCTCAGCAACGTTTGAACCGCTGAACAGCTGGC
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                                                                                       CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAATACG
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                 GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis strain H37Rv variant partial katG
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                                                                                                                                                                                                                                                                                                                                                                                      This partial DNA sequence encodes the katG gene from a variant strain of Mycobacterium tuberculosis H37Rv which is used in a novel method to rapidly identify strains of M. tuberculosis which are resistant to isoniazid (INH, also known as isonicotinic acid hydrazide). The method involves the use of restriction fragment length polymorphism (RFLP) analysis to determine if a Ncir-MspI restriction site is absent in the DNA of the strain at the codon corresponding to codon 463 of a M. tuberculosis katG gene consensus sequence (see AAW31343). The absence of the site indicates an INH-resistant strain.
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94US-0228662
                                                   94US-0228662
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us-09-674-277-1.rng

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event), both showing homology to the yeast enzyme, fused to a unic
N-terminal sequence of about 50 amino acid residues. Mutations in
the katG gene can result in loss of INH-susceptibility, i.e.
the formation of antibiotic resistant Mycobacterial strains
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                                                                                                             GATGGGCTTGGGCTGGAAGAGCTCGTATGGCACCGGAACCGGTAAGGACGCGATCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment by shotgun cloning. The sequence contains one open reading frame with high coding probability; a 735 amino acid protein is encoded by the ORF having predicted mol.w. 80029. This protein conforms to the structure of known bacterial catalase-peroxidases which consist of two modules (possibly the result of a duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The katG gene of Mycobacterium tuberculosis was isolated on a Kpnl
                                                                                                                                                                                                                                                                                 catalase-peroxídase; isonicotinic acid hydrazide; isoniazid; INH; antibiotic; susceptibility; sensitive; resistant; katG; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoniazid, rifampicin or streptomycin resistance in tuberculosis
by detecting mutation in katG, rpoB or rpsL genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rapid detection of antibiotic resistance in Mycobacteria -
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                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis (strain H37Rv).
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UNIV CURIE PARIS VI P &
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MEDICAL RES COUNCIL.
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Zhang Y;
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P-PSDB; AAR43670.
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14-AUG-1992;
16-APR-1993;
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                                         Query Match
18.4%; Score 274.2; DB 14; Length 4795;
Best Local Similarity 61.4%; Pred. No. 6.9e-78;
Matches 493; Conservative 0; Mismatches 303; Indels 7:
Sequence 4795 BP; 892 A; 1532 C; 1559 G; 812 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence encoding heat resistant peroxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ06815 standard; DNA; 2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89JP-0089469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         poD10; E.coli UM228; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR08205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ë,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   688 ATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGGAGGCTC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 TGAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGGATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATACAGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAACAGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encodes a catalase-peroxidase enzyme isolated from a M. tuberculosis
strain resistant to isonicotinic acid hydrazide (isoniazid or INH).
The sequence is useful in hed aliagnosis of tuberculosis caused by
INH-resistant M. tuberculosis and in the identification of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding catalase-peroxidase HPI - useful for rapid identification of isoniazid resistant Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                         isonicotinic acid hydrazide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents the Mycobacterium tuberculosis katG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4795 BP; 892 A; 1532 C; 1559 G; 812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                  Location/Qualifiers
1979. 4186
//tag- a //stag- a //gene- "atg"
/product- "catalase-peroxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 274.2; DB 20
Pred. No. 6.9e-78;
0; Mismatches 303;
                                                                          peroxidase; enzyme; isoni
diagnosis; resistance; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 10A; 46pp; English.
                                                                                                                                                                                                                                                                                                                                          95US-0459499.
92US-0875940.
92US-0929206.
93US-0029655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole ST, Heym B, Young DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.4%;
61.4%;
                                                                                                                                                                                                                                                                                                              95US-0459499
                                                                                                                      Mycobacterium tuberculosis,
              (first entry)
                                           M.tuberculosis katG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INH-resistant strains.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         PASTEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW78363
                                                                          ratG; catalase;
lsoniazid; INH;
                                                                                                                                                                                                                                                                                                                                                                                                                         ISNI ( dSNI)
             11-MAY-1999
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AAV06554 standard; DNA; 2262
                                    03-JUL-1998
                  AAV06554;
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                                                                                                                                                                                                                                                                                                                                                         GTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAAG 1086
                                                                                                                                                                                                                                                                                                                                                                                               ATGACTGGGAGTCG---GACCTGGTATACTGGGGGCCTGACAACAACCTCTTGCAGATA 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1322 AGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGG 1381
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                                                                                                                                                                                                                                                                                                                      GGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCTGACTG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                   1144 ACCGGGATAAAAACG--GGAAACTTCAGAAACCTCTTGCCGCCACGCAGATGGGACTTAT 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        896
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                                                                                                                                                                   AACAGCTGGATATGGAGGCTCTGAAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGG 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1202 TTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGGAAGCTTTTTCACGTATGGCCATGGATGATGAGGAGACTGTGGCCCTGATCGCGGG
                                                                                           CTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAACTCCTCTGA
                                                                                                                                GATTACACAGCCCTGAATCAAATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTC
                                                                                                                                                  ATCAACATGACCGAAAAACGAATCCTCATGATGAAGAGTTCAACTATGCTGAGGAGTTTC
                                                                                                                                                                                GTGCCGGAACATACAGGACATATGATGGCCGGGGAGGCGCCCAGTGGTGGTCAGCAACGTT
                                                                                                                                                                                                                                                        TTGAACCGCTGAACAGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGT
                                                                                                                                                                                                                                                                                                                                  664 CTACGTCAACCCAGAAGGGCCGGACGGCAAGCCGGATCCAAAAGCAGGGGGATATC---
                                                                          Gaps
                                                                         13;
be used to construct plasmid poD10 used to transfor. The transformed expression system may be used to
                                                       DB 11; Length 2196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1442 AAACGGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGAC 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 250.4; DB 11; Length
Pred. No. 2.5e-70;
0; Mismatches 351; Indels
                                    Sequence 2196 BP; 576 A; 564 C; 633 G; 423 T; 0 other;
                 produce heat resistant peroxidase in large quantities.
                                                       16.8%;
59.0%;
                                                  Query Match
Best Local Similarity 59.09
watches 524; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATTGCTGATGCCCGTGGGGGGGGGTACCGGAAGCCAGGGCTTTGCACGGCTCAACT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAAGAAAA 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is of the Alcaligenes aquamarinus catalase-64CA2 gene. Fragments of the gene can be used to identify related sequences. Catalase-64CA2 may be used to catalyse oxidation relations such as epoxidation or hydroxylation. The enzyme can also be used to detect or destroy hydrogen peroxide, e.g. in connection with glyoxylic acid production, biosensors, contact lens cleaning, pulp/paper bleaching and pasteurisation of dairy products. Antibodies raised against catalase-64CA2 can be used to screen libraries for detection and purification of cells containing the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCAGGTGCCGGAACATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              742 AGGCTCTGAAAAAGATATCAAAGATTTGCTGACAACTTCCCAGGATTGGTGCCCTGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  682 AATCAAATCCCTGGGGGGCTGATTTTGATTATGCCACCAGATTTCAACAGCTGGATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 AATCAGACCCGATGGATCCGGATTTCAACTACCGTGAAGAAGTACGCAAGCTCGATTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
                                                      epoxidation; hydroxylation; biosensor; paper bleaching;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.1%; Score 224.6; DB 19; Length 2262; 57.4%; Pred. No. 6.5e-62; tive 0; Mismatches 329; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New bacterial catalases, related nucleic acid vectors and transformed cells - used as oxidising agents and for detecting destroying hydrogen peroxide, e.g. in biosensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2262 BP; 553 A; 612 C; 663 G; 434 T; 0 other;
Alcaligenes (Deleya) aquamarinus catalase-64CA2 gene
                                                                                                                                                                                                                                                                           "Catalase-64CA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanyal I;
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RECO-) RECOMBINANT BIOCATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US16513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0674887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robertson DE,
                                                                                                                                                                                                                                               /*tag= a /product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                        Alcaligenes aquamarinus.
                                                                                                                                                                                                                     1..2262
/*tag=
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P-PSDB; AAW33809.
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                                                                                  pasteurisation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adhikary RS,
                                                                                                                                                                                                                                                                                                                                 WO9800526-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-1996;
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                                                        Catalase;
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13 RESULT 13

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WPI; 2000-431611/37.
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                                                                                ACCTGG---TATACTGGGGGCCTGACAACAAGCCTCTTGCAGAT-----TATACTGGGGGCCTGACAACAAGCCTCTTGCAGAT------1142
                                                                                                                                                                                                                 GAGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAG 1380
                                                                                                                                                                                                                                                 AATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAGAAGATGACTGGGAGTCGG 1101
                                                                                                                                                 TTTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATA 1260
                                                                                                                              GCGACGTGAACAAGCCAGAGACCATGGAAAACCGCTGGCGGCTGTCCAAATGGGTCTGA 757
                                                                                                                                                                                          CCTGGCCGGACAACGTCAGCCTGGATAAAGCGCGCCGTCTGCTGGGCCGATCAAGAAGA 517
                                                                                                                                                          982 AATACGGCTCCAGTATTTCCTGGGAGACCTGATGGTCCTGACTGGTAATGTTGCCCTTG
                           ---AACCGGGATAAAAACGGGAAACTTCAGAAACCTCTTGCCGCCACGCAGATGGGACTTA
                                                                                                                                                                                 TCAGGGAAGCTTTTTCACGTATGGCCATGATGAGGAGACTGTGGCCCTGATCGCGG
                                                                                                                                                                                                                                                             935 ACCCAAAAGCCTCTGACGTTGAAAACCAGGGCTTAGGTTGGGGGCAACCCCAACATGCAGG
                                                               578 AGTCCATGGGCTTACCTGCTTACGGCTTCTTTCGGCCGCCGCTATTTGGGAACCCG
                                                                                                GAAACGCCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGAC 1489
                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis katG gene (isoniazid resistance)
                                                                                                                                                                                                                                                                                                                                                                                                          Antibiotic resistance; katG gene; isoniazid resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "primer of AAA49827"
231..250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(41..60)
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                                                                                                                                                                                                                                                                                                                                         AAA49864 standard; DNA; 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0111794
                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer_bind
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                                                                                 1102
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AAA49864
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                                                                                                                                                                       The present sequence is that of the Mycobacterium tuberculosis katG (isoniazid resistance) gene (bp66-1320). Amplification and cycle sequencing primers (see AAAA9823-62) are used for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), proA (promycin), 165/rrs (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofiloxacin) and 233 (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB katG, rpsL/sl2 and 235 genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as to antibiotic treatment options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1395 CCTGTGGAGGAGCAGGGACTGGGATGGAAAATAAATGTGGGTACAGGAAACGGCAAATAT 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1215 GAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 CGGCGCATGGCCATGAACGACGTCGAAACAGCGGCGCTGATCGTCGCGGCGGTCACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 AAGCGGGATCTGGAGAACCCGCTGGCCGCGGTGCAGATGGGGCTGATCTACGTGAACCCG
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Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - {\sf Lober}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 660 BP; 127 A; 206 C; 227 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 122.8; DB 21;
Pred. No. 4.9e-29;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1455 ACCATCACCAGTGGCCTGGAAGGAGCCTGGTCGA 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 GCGATCACCAGCGGCATCGAGGTCGTATGGACGA 356
                                                                                                       Disclosure; Page 5-6; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium venenatum EST SEQ ID NO:13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.6%;
Matches 209; Conservative
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be contored. The expression of genes can be used to study how FF cells and pene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore on propagenesis, recombination, metabolic or catabolic or taponic or random cDNA clones including elimination of redundancy as one spot on an organisaris one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11857 represents ESTS from Aspergillus niger: AAF18679 represents ESTS from Aspergillus organisation in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCACCTGTGGAGGAGCAGGGACTGGGAAAAATAAATGTGGTACAGGAAACGCA 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1210 ATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCGAAAGATATCAGGGAAG 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 ATCACAACCGAGATCTCGAGAAGCCTTTGGCTGCTCACCACGGTCTCATGTTA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 CCTTCGGCCGATGGCCATGAACGACGAAAGACGCGTTGCTGTTGCTGGTGGTGGTGGTCACA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 CCGTCGGCAAGACCCACGGAGCTGGCTCAACCGACCA---CGTCGGCCCCGAGGCCCGAAG 382
                                                                                                                                                                                                                                                                                                                                                                                    Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
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                                                                                                                                                                                                                                                                                                       Clausen IG,
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Pred. No. 9.4e-20;
0; Mismatches 128;
                                                                                                                                                                                                                                                                                                       Berka RM, Rey MW, Shuster JR, Kauppinen S,
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                                                                                                                                                                                                                                     NOVO ) NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.4%;
                                                                                                                                                 22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                            99US-0273623
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                                                                                                                                                                                                                                                                                                                                             WPI; 2000-594572/56.
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                      Fusarium venenatum.
                                                               WO200056762-A2.
                                                                                                                                                                                            22-MAR-1999;
                                                                                                        28-SEP-2000
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a moilf 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calcutated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the centrain nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting multations or single nucleotide polymorphisms (SNR's); and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABO13410-ABO54121 represent genomic DNR sequences used to illustrate the method for determining the degree of cytosine methylation described in
383 CCGCCGACCTTGCCCAGCAGGGTCTCGGCTGGTCCAACAGCTACAAGACGGAAAGGGTCC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                                                                                                                                                                                                                                                                                                           Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                           Oligonucleotide for detecting cytosine methylation SEQ ID NO 9825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp; German.
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                                                                                                                                                                                               ВР.
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                               ABQ23234 standard; DNA; 538
                                                                                                                                                                                                                                                                                 (first entry)
                                          1450 AATATACCATCACCAG
                                                                                     443 GACACAACCACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                 12-JUL-2002
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1024 CIGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCTGGCGGAAGAG 1083

6.1%; Score 91.4; DB 24; Length 538; llarity 51.4%; Pred. No. 7.5e-19; Conservative 0; Mismatches 221; Indels 3:

Query Match Best Local Similarity Matches 237; Conserva

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Sequence 538 BP; 119 A; 47 C; 166 G; 206 T; 0 other;

the disclosure of the invention

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Gaps

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AAGATGACTGGGAGTCGGACCTGGTATACTGGGGGCCTGACAACAAGCCTCTTGCAGATA 1143
                                                                                                                                                                     ATGTCAATCCTGAAGGCCCCGGTGGAAACCAGATCCTCTGGCTTCCGCGAAAGATATCA 1263
                                                                                                                                                                                                                                GGGAAGCTTTTTCACGTATGCCCATGGATGATGAGGAGACTGTGCCCCTGATCGCGGGAG 1323
                                                                                                                                                                                                                                                                                            GGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGC 1383
                                                                                                                                      145 ATCGTTATTCGGAAGCGTTGGCGAAAGTATCGTTGGGTGTAATCGAGATGGGTTTGATTT 204
                                                                                                                                                                                                  ACGTTAATTCGGAAGGTTCGGATTATAGCGGCGAATCGTTTTTTGCGGGTAGTTATTC 264
                                                                                                                                                                                                                                                   382 TAGAAGTTGTATCGATTGAAGAATAAGGTTTAGGTTGGGCGAGTATTTACGGTAGCGGCG 441
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                AAGACGTTTGGGAATCGGATTTGGATGTTAATTGGGGTGATGAAAAAGTTTGGTTGATTT
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                                                                                                         ACCGGGATAAAAACGGGAAACTTCAGAAACCTCTTGCCGCCACGCAGATGGGAATTATTT
                                                                                                                                                                                                                                                                                                                        325 GTTATACGTTGGGTAAAATTTACGGTGTCGGTTCGATATTAAA---TGTAGGTTTTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present genomic sample of DNA. The sample is treated chemically to convert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide for detecting cytosine methylation SEQ ID NO 9826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis and proposits comprises selective hybridization is described.
                                                                                                                                                                                                                                                                                                                                                                                                                    1444 ACGCAAATATACCATCACCAGTGGCCTGGAAGGAGCCTGG 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                               442 TIGGCGIAGAIGITAITATITITIGGITIGGAAGIAGITIGG 482
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amplicons from chemically treated DNA
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2000DE-1044543.
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05-SEP-2000;
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cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the remember of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation of cell or tissue cypes and for investigating cell differentiation. The method allows the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 IAGAAGTTGTATCGATTGAAGAATAAGGTTTAGGTTGGGCGAGTATTTACGGTAGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                      Length 538;
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                                                                                                                                                                                                                                                                                                                                Sequence 538 BP; 206 A; 166 C; 47 G; 119 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                      DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 221;
                                                                                                                                                                                                                                                                                                                                                                  Score 91.4; DB 24
Pred. No. 7.5e-19;
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ilarity 51.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    fatches 237;
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                                                                                                                                                                                                                                                                                                                                                                                        Local
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RESULT 20
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                                                                                                                                                                                                                                                              The present invention relates to oligonucleotides based on nucleotide sequences obtained from both wild-type tubercle bacilli (wtTB) that are susceptible to a drug and mutant-type tubercle bacilli (mtTB) that are resistant to a drug and mutant-type tubercle bacilli (mtTB) that are resistant to a drug. The drugs used in the present invention are rifampicin (RFP), streptomycin (SM), kanamycin (KM), isoniazid (INH) and the mubber of EB). The present is responsible for resistance to RFF; the responsible for resistance to SM, the inhA gene is responsible for resistance to INH; resistance to SM, the inhA gene is responsible for resistance to INH; and the embB gene is responsible for resistance to INH; and the embB gene is responsible for resistance to INH; invention also relates to nucleic acid probes having part of a nucleotide sequence of tubercle bacilli (TB) responsible for drug resistance and primers used to generate the probes. The present sequence is an origination can be used to enable the differentiation of drug resistance and the determination of infection with tubercle bacilli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        852 GGAACATACAGGACATATGATGGCCGGGGAGGCGCCAGTGGTGGTCAGCAACGTTTTGAA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        912 CCGCIGAACAGCIGGCCGGAIAACGIIAAICIGGAIAAAGCCCGTCGAIIGCIGIGGCCA 971
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                                                                                                                                                                                       New oligonucleotides, nucleic acid probes and primers are useful for differentiating drug-resistance and determining infection with tubercle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGCACCTACCGCATCCACGACGGCCGCGGCGCCCGGGGGCGGCATGCAGCGGTTCGCG
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streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs gene;
rpsL gene; inhA gene; katG gene; embB gene; probe; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 150 BP; 29 A; 51 C; 53 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75.6; DB 22
Pred. No. 4.9e-14;
0; Mismatches 39
                                                                                                                                                                                                                                        Disclosure; Page 61-62; 114pp; English.
                                                                                                                                        Takenishi S;
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71.78;
                                                02-AUG-2000; 2000EP-0306563
                                                                           99JP-0220357
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                                                                                                   NISN ) NISSHINBO IND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99; Conservative
                                                                                                               (SYST-) SYSTEM RES INC.
                                                                                                                                        Suzuki Y, Nishida M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                WPI; 2001-246696/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       simultaneously.
EP1076099-A2
                                                                        03-AUG-1999;
                       14-FEB-2001.
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The present invention relates to oligonucleotides based on nucleotide sequences obtained from both wild-type tubercle bacilli (wtTB) that are susceptible to a drug and mutant-type tubercle bacilli (mtTB) that are resistant to a drug and mutant-type tubercle bacilli (mtTB) that are resistant to a drug. The drugs used in the present invention are rifampicin (RFP), streptomycin (SM), kananycin (KM), isoniazid (INH) and thambutol (EB). The rpoB gene is responsible for resistance to RPP; the rs gene is responsible for resistance to SM; the linh gene is responsible for resistance to INH; and the embB gene is responsible for resistance to INH; and the embB gene is responsible for resistance to INH; cand the embB gene is responsible for resistance to INH; invention also relates to nucleic acid probes having part of a nucleotide sequence of tubercle bacilli (TB) responsible for drug resistance and primers used to generate the probes. The present sequence is an prigonucleotide of the present invention. The oligonucleotides of the present invention can be used to enable the differentiation of drug resistance and the determination of infection with tubercle bacilli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligonucleotides, nucleic acid probes and primers are useful for differentiating drug-resistance and determining infection with tubercle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          962 GCTGTGGCCAGTCAAGAAAAATACGGCTCCAGTATTTCCTGGGGAGACCTGATGGTCCT
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                                                                      02-AUG-2000; 2000EP-0306563.
                                                                                                                                                 99JP-0220357
                                                                                                                                                                                                                           (NISN ) NISSHINBO IND INC.
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Best Local Similarity 65.38
Matches 98; Conservative
                                                                                                                                                                                                                                                                       (SYST-) SYSTEM RES INC.
                                                                                                                                                                                                                                                                                                                                         Suzuki Y, Nishida M,
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-246696/26.
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                                                                                                                                                 03-AUG-1999;
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14-FEB-2001.
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WO200218632-A2.

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SNP; cell differentiation;
                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invariant states to originate clauses make on universective sequences obtained from both wild type tubercle bacilli (wtTB) that are susceptible to a drug and mutant-type tubercle bacilli (wtTB) that are susceptible to a drug. The drugs used in the present invention are rifamptoin (RPP), streptomycin (SM), kanamycin (KM), isoniazid (INH) and ethambutol (EB). The rpoB gene is responsible for resistance to SM and KM; the rpsL gene is responsible for resistance to SM; the inhA gene is responsible for resistance to SM; the inhA gene is responsible for resistance to INH; and the embB gene is responsible for resistance to INH; and the embB gene is responsible for resistance to INH; and the embB gene is responsible for resistance and invention also relates to nucleic acid probes having part of a nucleotide sequence of tubercle bacilli (TB) responsible for drug resistance and colligonucleotide of the present invention can be used to enable the differentiation of drug resistance and the determination of infection with tubercle bacilli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793 GCCCTGCGGGATTATGGTCATTATGGTCCTTTATTCGTATGGCTTGGCACGGTGCCG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 regaectreacecereacecegacarcageaagreargaceacerecage 71
                                                                                                                                                                                                                                                                                                  New oligonucleotides, nucleic acid probes and primers are useful for differentiating drug-resistance and determining infection with tubercle bacilli .
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to oligonucleotides based on nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63.8; DB 22; Length 150;
Pred. No. 3.4e-10;
0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 150 BP; 26 A; 53 C; 48 G; 23 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 61; 114pp; English.
                                                                                                                                                                                                                                               Takenishi S;
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                                                                                                          02-AUG-2000; 2000EP-0306563
                                                                                                                                                  99JP-0220357
Mycobacterium tuberculosis.
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Best Local Similarity 66.2*
                                                                                                                                                                                     (NISN ) NISSHINBO IND INC (SYST-) SYSTEM RES INC.
                                                                                                                                                                                                                                               Suzuki Y, Nishida M,
                                                                                                                                                                                                                                                                                  WPI; 2001-246696/26.
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                                 EP1076099-A2
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cc This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cc cytosine (c) but not methylated c, to uracil, then part of the genomic DNA that contains the target c is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one cmember, of oligomets the mad/or peptide-nucled: acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two cc classes of oligomers the degree of methylation is calculated. The method is used: (i) for diagnosis and/or progness; of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (il) for differentiation of call or tissue contypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Ampliation status of many C residues to be determined simultaneously. The disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AATCTAATTTACGTTAACCCGAAAAACCCGAATCACAACGACGAACCGCTTTCTACGACA 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1014 ATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the degree of cytosine methylation in genomic DNA, of diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
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45.9%; Pred. No. 0.00017;
tive 0; Mismatches 191; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                         Berlin K,
                                                                                                                                                                 01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                            01-SEP-2001; 2001WO-EP10074
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                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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07-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                         olek A,
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1074 GGCGGAAGAGAAGATGACTGGGAGTCGGACTGGTATACTGGGGGCCTGACAACAAGCCT 1133

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Method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
Oligonucleotide for detecting cytosine methylation SEQ ID NO 9828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                BP
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                ABQ23237 standard; DNA; 538
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                                                                                                                                                     RESULT 22
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The present invention relates to oligonucleotides based on nucleotide sequences obtained from both wild-type tubercle bacilli (wtTB) that are susceptible to a drug and mutant-type tubercle bacilli (wtTB) that are resistant to a drug and mutant-type tubercle bacilli (wtTB) that are resistant to a drug and mutant-type tubercle bacilli (wtTB) that are resistant to a drug. The drugs used in the present invention are resistant (EM), streptomycin (SM), kanamycin (KM), isoniazid (INH) and thambutol (EB). The rpoB gene is responsible for resistance to SRP; the responsible for resistance to SM; the inhA gene is responsible for resistance to INH; the katd gene is responsible for resistance to INH; can the embB gene is responsible for resistance to EB. The present invention also relates to nucleic acid probes having part of a nucleotide sequence of tubercle bacilli (TB) responsible for drug resistance and primers used to generate the probes. The present sequence is an oligonucleotide of the present invention. The oligonucleotides of the present invention be used to enable the differentiation of drug
                                                                             1194 GGACTTATTTATGTCAATCCTGAAGGCCCCGGTGGAAAACCAGATCCTCTGGCTTCCGCG 1253
                                                                                                                                                      1254 AAAGATATCAGGGAAGCTTTTTCACGTATGGCCATGGATGATGAGGAGACTGTGGCCCTG 1313
1134 CTTGCAGATAACCGGGATAAAACGGGAAACTTCAGAAACTTGTGCCGCCACGCAGATG 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a nucleotide
                        ACAACTATCCGCGCGCGACCTTCGACAACATAAACGACGAAAAAAACGGTAACGCTA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligonucleotides, nucleic acid probes and primers are useful for differentiating drug-resistance and determining infection with tubercle bacilli -
                                                                                                               195 AATCTAATTTACGTTAACCCGAAAAACCCGAATCACAACGACGAACGCTTTCTACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tubercle bacillus; drug sensitivity; drug resistance; rifampicin; streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs gene; rpsL gene; inha gene; katG gene; embB gene; probe; PCR primer; ss.
                                                                                                                                                                                                                                   ATCGCGGGAGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAA 1366
                                                                                                                                                                                                                                                           Disclosure; Page 62; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                     AAF95162 standard; DNA; 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISN ) NISSHINBO IND INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-246696/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      katG gene probe #4.
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                                                                                                                                                                                                                                   1314
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Gaps

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Score 47.4; DB 24; Length 538; Pred. No. 0.00017; 0; Mismatches 191; Indels 0

3.28;

Query Match 3.29 Best Local Similarity 45.99 Matches 162; Conservative

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1014 ATGGTCCTGACTGGTAATGTTGCCCTTGAATCCATGGGATTTAAAACGCTGGGATTTGCT 1073 ATTATCCTCGCGAATAACGTAAAGGCTAAAAAACTCCGGACTTCCGTACCTTCGATTTTAAT 74

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WPI; 1997-425040/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-1998
                                                                                                                                                                                                                   Matches 100;
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                                                                                                                                                                                            Query Match
Best Local
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                                                                                                              1260 ATCAGGGAAGCTTTTTCACGTATGGCCATGGATGATGAGGAGACTGTGGCCCTGATCGCC 1319
                                                                                                                                                                 1320 GGAGGGCATACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCA 1379
                                                                                         ä
                                                                                                                                                                                        62 GGCGGTCACACTTTCGGTAAGACCCATGGCGCCGGCCCGGTCTGG---TCGGCCCC 118
                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the Fr cells and a substrate of expressed sequence tags (EST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microcorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus Oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olsen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for monitoring differential
resistance and the determination of infection with tubercle bacilli
                                                              Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clausen IG,
                                                              Score 46.4; DB 22; Length
Pred. No. 0.00016;
0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Multiple gene expression; filamentous fungal cell; EST;
                                    Sequence 150 BP; 26 A; 49 C; 51 G; 24 T; 0 other;
                                                                                                                                                                                                                 1380 GGCCTGATGGTGCACCTGTGGAGGAGCAGGG 1411
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                                                                                                                                                                                                                                Kauppinen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 88; Page 1893-1894; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae EST SEQ ID NO:4432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                          BP
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                                                                                       ;
                                                                                                                                                                                                                                                                                                      AAF11909 standard; cDNA; 1358
                                                               3.1%;
                                                                         llarity 61.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2000; 2000WO-US07781.
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                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae.
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              simultaneously
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                                                                                       93;
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                                                              Query Match
                                                                            Local
                                                                            Best Loc
Matches
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adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway morphogenesis, recombination, metabolic or catabolic pathway engineering using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on a array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF01478 to AAF11247 represents ESTs from Aspergillus niger; AAF11861 to AAF118678 represents ESTs from Aspergillus oryzae; and AAF18679 to AAF118678 represents ESTs from Aspergillus oryzae; and all specifically claimed in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        801 GATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAACATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   861 AGGACATATGATGGCCGGGGAGCCCCAGTGGTGGTCAGCAACGTTTTGAACCGCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
The expression of genes can be used to study how FF cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPRP-F1; tomato fruit expressed proline-rich protein gene; ovary; promoter; genetic parthenocarpy; auxin modulator; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                           Length 1358;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                     Sequence 1358 BP; 258 A; 430 C; 348 G; 322 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                     Score 38.8; DB 21;
Pred. No. 0.19;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPRP-F1 gene, including the promoter region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              981 AAATACGGCTCCAGTATTTCCT 1002
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                                                                                                                                                                                                                                                                                                                                                                                           2.6%;
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2235..4320
/*tag= b
2644..3684
/*tag= c
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23-MAR-2001; 2001WO-US09231.

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3807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            808 AAATATITIGATITATACTACTIAITACGTAGTTITCATAAGTATAAATITCATTACATA 3867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               723
                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 CTTAGTATTTTTGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3748 AGTTGACAFTTCAAGTATTAGGCCCAAFTTTTCTTAGCTCGGAAFTTTTTTAAATCTCTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664 TGAGATTACACAGCCCTGAATCAAATCCCTGGGGGGCCTGATTTTGATTATGCCACCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3868 TATGAATTCACGGTCAAAATTTAAAGTTTAATTTAACCAATGCCACATAACTTAGAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724 TICAACAGCIGGAIAIGGAGGCICIGAAAAAAGAIAICAAAGAITIGCIGACAACIICCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 AAGTIGACITITGIATACAACAIGCGAAITICCCITAAICCGGAGCIATICGIAIGAIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 AAAAAACTCTTCCTGTTCTGATTCTTCTGGCGCTATCGGGGAGCTTTTCTACCGCTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604 CCGCTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAACTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                              This sequence comprises a genomic clone of the tomato fruit expressed proline-rich protein gene TPRP-F1, including the promoter region. A claimed method for the production of genetic parthenocarpy in plants comprises: providing a cassette including DNA coding for modulation of auxin effects in plants and a promoter specific for the ovary between anthesis and early fruit development, and introducing the cassette into a plant. Suitable promoters include the TPRP-F1 promoter and an alternative TPRP-F1 promoter see AATB9279) that confers ovary and developing embryo specificity. The method allows parthenocarpy to be induced in especially tomato plants without the need to apply (synthetic)
           Producing genetic parthenocarpy in plants - with sequence encoding auxin modulator controlled by promoter specific for the ovary
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                                                                                                                                                                                                                                                                                                                                          Sequence 4320 BP; 1450 A; 844 C; 585 G; 1441 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             Score 38.8; DB 18;
Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 217;
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                                                                     Claim 7; Fig 9; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                               2.6%;
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Best Local Similarity
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1329 ACATTTGGTAAAGCACATGGTGCAGCGTCTCCTGAAAAATGTATTGGCGCAGGGCCTGAT 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5591;
                                                                                                                                                                                                                   Claim 1; SEQ ID NO 20621; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5591 BP; 1876 A; 1209 C; 1357 G; 1149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.8; DB 23;
Pred. No. 0.99;
0; Mismatches 52;
                                                                                            Myers EW;
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                                                                                              PWD,
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11-JUL-2000; 2000US-0614150.
                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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Best Local Similarity 57.0
Matches 69; Conservative
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                                                                                            Venter JC, Adams M,
                                                                                                                     WPI; 2001-656860/75.
P-PSDB; ABB64610.
                                                                  (PEKE ) PE CORP
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Lathigra R,

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426 TAGTATTTTTTGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Borrelia belongs to a family of mottle, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                          New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                    Sequence 14752 BP; 5196 A; 1781 C; 1634 G; 6139 T; 2 other;
                                                                                                                                                   Claim 1; Page 893-901; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                Query Match 2.5%;
Best Local Similarity 57.4%;
Matches 66; Conservative (
                  Dougherty BA,
                                                             WPI; 1999-081217/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusarium venenatum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-1999;
                                                                                                                                                                                                                                                                                                       Lyme disease
               Clayton R,
White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention 1 useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 6000;
                                                                                                                                                              Claim 1; SEQ ID NO 20447; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 6000 BP; 2026 A; 1274 C; 1434 G; 1266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi polynucleotide sequence #9.
                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                           Score 37.8; DE Pred. No. 1; 0; Mismatches
                               Myers EW;
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                               PMD,
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97US-0050359.
97US-0053344.
97US-0053377.
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(MEDI-) MEDIMMUNE INC.
                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrella burgdorferi
                                                          WPI; 2001-656860/75.
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(PEKE ) PE CORP NY.
                                                                          P-PSDB; ABB64552
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                                                                                                                                    Interactions -
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Matches
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8163

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Gaps

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Indels

49; DB 20;

Score 36.6; DB; Pred. No. 4.5; 0; Mismatches

Length 14752;

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Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
Olsen PB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple gene expression; filamentous fungal cell; EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium venenatum EST SEQ ID NO:273.
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                                                                                                                                                                                                                                                                                                                                         AAF07750 standard; cDNA; 801
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Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

Claim 8; Page 477; 2188pp; English.

(GLAX) GLAXO GROUP LID

WPI; 2001-316495/33 P-PSDB; AAG82315

Kimmerly WJ;

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cells. The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be discovered, the expression of genes can be used to study how FF cells and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway complementing. Using ESTS provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an increarrays based on function of the gene products to facilitate analysis of the results. AAF01478 to AAF11877 represents ESTS from Aspergillus oryzae; and pressit, which are all and an are the conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        all specifically claimed in the present invention.
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Best Local Similarity 49.7%; Pred. No. 0.84;
Matches 91; Conservative 0; Mismatches 92;
                 Claim 86; Page 488; 3161pp; English
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AAH55304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to raise antibodies against the bacteria. The polypeptides may also be used to casay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA parences the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 GCTGTAGCCGCTGATAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTA 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 22; Length 327;
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0; Mismatches
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AAH54197 standard; DNA; 3803 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccination; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200134809-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH54197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 8
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ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(II) and (II) can have antibacterial activity and therefore can be used.

(I) and (II) can have antibacterial activity and therefore can be used.

(I) and (II) can have antibacterial activity and therefore can be used.

(I) and (II) can be used to produce the produce the state of the polypeptides (II) via the production of vectors.

(I) and them which are used to produce hosts cells which express the polypeptides way also be used to raise antibodies against the bacteria.

(I) and therefore acids in a constant the bacteria.

(I) and therefore acids in the constant is antibodies against the bacteria.

(I) and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to AAH55098 represent oil gonucleotide sequences and primers which are used in the exemplification of the present invention.

(I) The prosent invention specifically claims all the polymucleotide sequence listing of the present specification, however the sequence listing of the present specification, however the sequence listing of the present specification.

(I) though sequence listing only goes up to SEQ ID NO:4455 to 4772, and the present specification are not accompanies and primers for SEQ ID NO:4455 to 4772, and the present specification are not accompanies and primers and primers and primers are specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 GCTGTAGCCGCTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                695 GATTTAAACGATGATTTTGAAGATTCTTTAGAGTATTTGGAGCCATTAGATCATGATGCA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               657 ACTCCTCTGAGATTACACAGCCCTGAATCAAATCCCTGGGGGGGCTGATTTTGATTATGCC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635 TATATTGTGAGGTTAAACTTTACTGGTGAAATACGACTGAGCCTATCATATCTTATATG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                            Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 3803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3803 BP; 1329 A; 547 C; 681 G; 1246 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #8814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4%; Score 35; DB; 50.3%; Pred. No. 6.4; Live 0; Mismatches
                                                                                                                                                                                                                                                                               Claim 8; Page 1145-1146; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS73010 standard; cDNA; 824
                      99US-0164258
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                                                                   (GLAX ) GLAXO GROUP LID
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Best Local Similarity
Matches 86; Conserva
                                                                                                                                                               WPI; 2001-316495/33
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                      09-NOV-1999;
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                                                                                                                  Kimmerly WJ;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AsS64197 AsS6445 represent novel human when the polypeptide and polymetion in an invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           917 GAACAGCTGGCCGGATAACGTTAATCTGGATAAAGCCCGTCGATTGCTGTGGCCAGTCAA 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797 IGCGGATTATGGTCATTATGGTCCTTTCTTTATTCGTATGGCTTGGCACGGTGCCGGAAC 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCCGTGGTGGCGACAAACGCGGTGGTGCCAACGGTGCGCGTCTGGCATTAATGCCGCA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TGCGGATTCTGGTCTGTTAGTGAGCTGGTATCGGTGGCCTGGGCATCTGCTTCTAC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34.8; DB 23;
Pred. No. 2.9;
0; Mismatches 122;
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                                                                                                                                                         Tang YT;
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Best Local Similarity 49.2%;
Matches 121; Conservative
30-MAR-2001; 2001WO-US08631
                                         31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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251 TGTTGA 256
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                                                                                                           HYSE-) HYSEQ INC
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ID AAS90
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AC AAS90
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977 GAAAAATACGGCTCCAGTATTTCCTGGGAGACCTGATGGTCCTGACTGGTAATGTTGC 1036
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                                                                                                                                                1037 CCTTGA 1042
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AAK55269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                857 ATACAGGACATATGATGGCCGGGGGGGCGCCAGTGGTGGTCACCAACGTTTTGAACCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; dlagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6240 BP; 1491 A; 1747 C; 1604 G; 1398 T; 0 other;
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                                                                                                                     DNA encoding novel human diagnostic protein #25942.
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Pred. No. 10;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 25942; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                              13-FEB-2002 (first entry)
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Best Local Similarity
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P-PSDB; ABG25951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-0CT-2001.
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:329,
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2000US-0233063
                                                                                              2000US-0249218
                                                          08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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aniho acid sequences given in AMM81210 to AAM891921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own produce the secreted (I), by inserting polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK44942 to AAK87694 represent invention. AAK44942 to AAK87595 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 GCTATTCGTATGATAAAAAACTCTTCCTGTTCTGATTCTTCTGGCGCTATCGGGGAGC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I
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Pred. No. 2.5;
0; Mismatches 65; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM
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Best Local Similarity 52.9%;
Matches 73; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                           20000S-0249300
20000S-0250160
                                                                                                                                                                                2000US-0251988
2000US-0256719
                                                     2000US-0249265
2000US-0249297
                                                                                        2000US-0249299
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                                                                                                                                               2000US-0250391
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P-PSDB; AAM82488.
                                                                                      17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
                                17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                 05-DEC-2000;
                                                                                                                                           01-DEC-2000;
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588 ITTTCTACCGCTGTAGCCGCTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACA 647

648 CIGGATITAACICCICIG 665 TTTCCTTAGCCACTTCAG 504

487

RESULT 35 ABL70580/c

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Human gene regulation-associated gene oligonucleotide #216.
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Matches
g
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                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid comprising a sequence of at least bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonuclectides and/or PNA-oligomers for detecting cytosine methylations, as well as method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL/0111-ABL/0626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling.

Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 TAICTAICCCAGCAATAGGIAIATCCIGIIGCAICAATAAAGIIGACIITIGIAIACAAC 504
                                                                                                                                                                                                                                                                                                                                             Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                        Chemically treated cell signalling DNA sequence complementary to#235
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                                                                                                Cell signalling; cytosine methylation; cell signalling disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Score 34.6; DB 24; Length 6065; 58.1%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 ATGCGAATTTCCCTTAATCCGGAGCTATTCGTATGATAAAAAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6065 BP; 1602 A; 178 C; 1473 G; 2812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 470; 24pp+sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                             with cell signalling e.g. cancer, comprises chemica sequences of genes associated with cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                 Berlin K;
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                                                                                                             cancer; tumour; cytostatic; ds
 ABL70580 standard; DNA; 6065
                                                                                                                                                                                                             29-JUN-2001; 2001WO-EP07471
                                                                                                                                                                                                                                   30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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                                                  (first entry)
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                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                        WPI; 2002-154758/20
                                                                                                                                                             WO200202807-A2.
                                                  01-JUL-2002
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                                                                                                                                    Unidentified
                                                                                                                                                                                    10-JAN-2002.
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                         ABL70580;
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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the chemical pretreatment converts cytosine bases unmethylated at the chemical pretreatment converts cytosine bases unmethylated at the chemical pretreatment converts cytosine bases unmethylations. Consistent of the cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/Arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, conditing analysis of the cytosine methylation patterns of such diseases, and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, cardiac disorders, patching in the sequence data for this specification and is sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes.

Conce: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form that directly from WIPPO at the printed specification, but was obtained in electronic
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                                      cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; oclorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coaquiant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 TATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAAGTTGACTTTTGTATACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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AAZ42098 standard; cDNA; 544

AAZ42098;

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RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, blopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK1158-ABK11545 represent chemically pretreated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 TATCTATCCCAGCAATAGGTATATCCTGTTGCATCAATAAAGTTGACTTTTGTATACAAC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences of different genes associated with signal transduction, or their complementary sequences.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                   Signal transduction associated gene modified complementary DNA #100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 ATGCGAATTTCCCTTAATCCGGAGCTATTCGTATGATAAAAAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6065 BP; 1602 A; 178 C; 1473 G; 2812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 200; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
              ABK31357 standard; DNA; 6065 BP
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1larity 58.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001; 2001WO-EP07472
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-147896/19
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es 61; Conserv
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                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                           23-APR-2002
                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                                                            Synthetic.
                                                      ABK31357;
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ABK31357,
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This invention describes novel human nucleic acid (cDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (1) for recombinant expression of polypeptides (B) and (11) to isolate complete genes. (B) are used (1) to identify agents suitable for treatment of uterine or anometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly inder fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent frequency of occurrence in a particular tissue. AAA41981-242121 represent EST fragments derived from a human endometrium tumour cDNA 11brary which encode the protein sequences represented in AAY59941-Y60328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        534 TGGTGATCAAATTAACCTTCAGGTCCTTTCTCCTCCTGGAAAGCACTCTACTGCTTCAA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 CAGGTCCAAGCTGCCATCGCCTCTTTTCTGAGTGATTGCAATAGCCCTATCAGGTTTCCA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 TATATCCTGTTGCATCAATAAAGTTGACTTTTGTATACAACATGCGAATTTCCCTTAATC 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dahl E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 TGTTTCTGACATCCACAAAGAAGGGAATATTCAGGTCTGCGCAGCACTCAACGGCATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents
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Pred. No. 3;
                                                                                                                                                              Endometrium; human; tumour; cancer; anticancer; cytostatic; E:
treatment; uterine; gene therapy; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 146; Indels
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                                                                                 Human endometrium tumour cDNA derived EST 118,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-591957/51.
P-PSDB; AAY60301, AAY60302, AAY30303.
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Best Local Similarity 47.5%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-1017948
                                                                                                                                                          Endometrium; human; tumour;
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31-JAN-2000
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peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell cancerous, where the gene product is encoded by one of the 5248 polynuclectide sequences given in AAZ12532 to AAZ1779. The polynuclectides can be used as a source of primers and probes, which can be used for availety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer. The polynucleotides can also be used to screen for and lung cancer. The polynucleotides can also be used to screen for
                                     354 CIGCTGTTTGCCATGGCTCAATAAATTCCTTGAGTTCTGGCCCTAAAGACTCTCGCTGG 295
        524 CGGAGCTATTCGTATGATAAAAAAACTCTTCCTGTTCTGATTCTTCTGGCGCTATCGG
                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                Human gene expression product cDNA sequence SEQ ID NO:2644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                               294 eccrerrecacceaagacacaagacagacagacagarer 255
                                                                                          584 GAGCTTTTCTACCGCTGTAGCCGCTGATAAAAAGAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1286; 2479pp; English.
                                                                                                                                                                                                                                         AAZ15175 standard; cDNA; 800 BP
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98US-0072910.
98US-0075954.
98US-0080114.
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(HYSE-) HYSEQ INC
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24-FEB-1998;
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03-APR-1998;
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                                                                                                                                                                                                                                                                                   AAZ15175;
                                                                                                                                                                                                 RESULT 39
                                                                                                                                                                                                                       AAZ15175,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are ischerichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aerupinosa and Enterococcus faecalis. The pneumoniae, Pseudomonas aerupinosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for for antibiotic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense
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                                                                                                                                                                                                   793 ITAAACCTAGCCNCAGGTTTTCCCCNTGTCACCNAGACTGGAGTTAAGAANCCTGANAAN 734
                                                                                                                                                                                                                                                       611 TAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAACTCCTCTGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus cellular proliferation inhibitory sequence #835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr GJ;
                                                                                                   Gaps
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                                                 DB 20; Length 800;
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                                                                                                   Indels
  other;
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25
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Sequence 800 BP; 255. A; 153 C; 158 G; 209 T;
                                                                       Pred. No. 4.4;
0; Mismatches
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                                                    Score 34.2;
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Xu HH;
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2000US-206848P.
2000US-207727P.
2000US-25362P.
2000US-25362P.
2000US-25362P.
2001US-269308P.
                                                 ch 2.3%;
1 Similarity 53.4%;
63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
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Yamamoto RT,
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27-NOV-2000;
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23-MAY-2000;
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Best Local S
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us-09-674-277-1.rng

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27-SEP-2001
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                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Entercoccus faccalis. The invention is also useful for the identification of potential new targets
                                                                                                                          483 AAAGTTGACTTTTGTATACAACATGCGAATTTCCCTTAATCCGGAGCTATTCGTATGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr GJ;
                                                                                            Gaps
                                                                                                                                                                                             GCCGCTGATAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAA 657
                                                                                                                                                                                                          Staphylococcus aureus DNA for cellular proliferation protein #1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                       DB 23; Length 893;
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick JD,
                                                                                         88; Indels
                                                                                                                                                                                                                                                                                                                                                  Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                  Sequence 893 BP; 273 A; 161 C; 119 G; 340 T; 0 other;
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                                                                     Query Match
2.3%; Score 34.2; DE
Best Local Similarity 49.7%; Pred. No. 4.7;
Matches 87; Conservative 0; Mismatches
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                               ftp.wipo.int/pub/published_pct_sequences
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Xu HH;
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200005-207727P
200005-242578P
200005-255625P
200005-25762P
200105-25763P
200105-269308P
                                                                                                                                                                                                                                                                   AAS55352 standard; DNA; 927
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                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                       AAS55352;
                                                                                                                                                                                                                                                RESULT 41
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for antiblotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    542
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 GCCGCTGATAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus DNA for cellular proliferation protein #667.
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                                                                                                                                                                                                                                                                                                                                                           Length 927;
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                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                           Sequence 927 BP; 347 A; 116 C; 169 G; 295 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wall D,
                                                                                                                                                                                                                                                                                                                                                      Score 34.2; DE
Pred. No. 4.8;
0; Mismatches
                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS52250 standard; DNA; 1164 BP
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20000S-207727P.
20000S-242578P.
20000S-253625P.
2000US-257931P.
                                                                                                                                                                                                                                                                                                                                                      Query Match 2.3%;
Best Local Similarity 49.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                    87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
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27-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
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26-MAY-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes themselves and the discovery of novel antiblotics, the essential genes themselves and the discovery of novel antiblotics, the essential genes themselves and the discovery of novel antiblotic and seed and Entercoccus faecalis. The prention is also useful for the identification of potential new targets for antiblotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to soreen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part for the printed specification, but was obtained in electronic format directly from WIPO at the printed protablished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483 AAAGTIGACITITGIATACAACATGCGAATTITCCCTTAATCCGGAGCTATICGIATGATA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 GCCGCTGATAAAAAAGAGACTCAAAATTTCTACTATCCAGAAACACTGGATTTAA 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.3%; Score 34.2; DB 23; Length 1164; Best Local Similarity 49.7%; Pred. No. 5.6; Matches 87; Conservative 0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1164 BP; 426 A; 164 C; 203 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus contig SEQ ID #565.
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1561..1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV74876 standard; DNA; 2554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0009861
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/note= "t]
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are itself to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including calvillitis, eyelld infections, food poisoning, osteomyelitis, synfrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences of any of the S.aureus DNA sequences con tisolating computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 AAAAAACTCTTCCTGTTCTGATTCTTCTGGCGCTATCGGGGAGCTTTTCTACCGCTGTA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 98P6G3; ss; homeodomain protein; vaccine; cytostatic.
epitope; transgenic animal; immunogen; T cell; B cell; cytotoxic T cell;
CTL; prostate cancer; bladder cancer; kidhey cancer; lung cancer;
breast cancer; uterine cancer; cervical cancer; stomach cancer;
rectal cancer; colon cancer; chromosome 4q11-q12; PCR primer; adapter;
suppression subtractive hybridisation; SSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 ATAATITITITAATITAATCTGGTTCTTCAGTAGCACTTGTCACGATTGAAAAACTATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 AAAGTTGACTTTTGTATACAACATGCGAATTTCCCTTAATCCGGAGCTATTCGTATGATA
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                                                                                                                               Polynucleotide(s) and proteins derived from Staphylococcus aureus
stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2554;
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                                 Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA fragment for cancer related protein 98P7C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2554 BP; 793 A; 433 C; 328 G; 933 T; 67 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18;
                                   Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34.2; DI
Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                        Claim 1; Page 1503-1504; 3271pp; English.
                                   Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS99435 standard; cDNA; 188 BP.
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(HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 49.7 nes 87; Conservative
                                                                                                                                                                      anti-S.aureus vaccines
                                   Choi GH,
                                                                                           WPI; 1997-374922/35.
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                                   Barash SC,
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                                                       Rosen CA;
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Matches
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29-NOV-2001

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Human foetal cDNA, SEQ ID NO: 1179.
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Zhou P, W
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06-NOV-2000; 2000US-0707351.
                                                                                                                                                                                                                                 25-JAN-2001; 2001WO-US02723
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Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
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                                                                                                                                                                 WO200155339-A2.
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                                                                                                                                                                                                                                                                                                                                                                       polynuclectides) or a host cell transformed with the vector, an anti-98P7C3 antibody, an non-human transgenic animal expressing a anti-98P7C3 antibody, an non-human transgenic animal expressing a superior of special mainly an anti-98P7C3 protein or polynuclectides in a biological sample, monitoring the presence of cancer in an individual by detecting an elevated level of the 98P7C3 protein or polynuclectides and a pharmaceutical composition comprising a modulator of 98P7C3. 98P7C3 protein, or T cell/B cell epitopes derived from it, are useful in inducing an immune response (in mammal) to a 98P7C3 protein. Upon contact with a cytotoxic T cell (CTL) the immunogens induce the CTL (with its helper T cell) to kill an autologous cell expressing 98P7C3. The immunogen may be a nucleic acid encoding the protein or epitope. The antibody is useful for delivering a cytotoxic agent to a cell that expresses 98P7C3, by conjugating the cytotoxic agent to the antibody or its fragment that specifically binds to a 98P7C3 epitope, and exposing the cell to the antibody-agent conjugate. The modulator is useful for treating a patient with a cancer that expresses 98P7C3 epitope, the suseful for reacting a patient with a cancer, lung cancer, breast cancer, uterine cancer, cervical cancer, rectal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 TAGGTATATCCTGTTGCATCAATAAAGTTGACTTTTGTATACAACATGCGAATTTCCCTT 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is oligonucleotide adapter or PCR primer used to isolate a cDNA sequence for 98P7C3 by the method of suppression subtractive hybridisation, SSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 TNAGTITATITIGNINAATAAANTGAACTGCTTTTTGTCTCTAAAATNATNTTTTNAATN 54
                                                                                                                                                                                                                                                                                          The invention relates to an isolated 98P7C3-related protein which is a homeodomain protein highly expressed in various cancers. Also include are polynucleotides encoding the protein or proteins 90% identical to 98P7C3, a pharmaceutical composition comprising the polynucleotides (including an expression vector comprising the 98P7C3 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer and colon cancer), by administering to the patient a vector that comprises the modulator, such that the vector delivers a single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain atthody is expressed intracellularly in it.

The gene for 98P7C3 is located on human chromosome 4q11-q12. The prese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                           New isolated 98P7C3-related homeodomain protein highly expressed in various cancers, useful in cancer vaccines and for generating immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 24; Length 188;
Pred. No. 2.1;
0; Mismatches 38; Indels
                                                                                                               Afar DEH, Levin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 188 BP; 55 A; 19 C; 15 G; 80 T; 19 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Faris M,
                                                                                                                                                                                                                various cancers, useful in cancer vac
response directed to 98P7C3 in mammal
                                                                                                                                                                                                                                                              Example 1; Fig 1; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      вР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH94492 standard; cDNA; 308
                                                                                                              Challita-Eid PM, Hubert RS, Mitchell SC, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.8%;
               24-MAY-2001; 2001WO-US17495
                                                24-MAY-2000; 2000US-207138P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Conservative
                                                                                (UROG-) UROGENESYS INC
                                                                                                                                                              WPI; 2002-097642/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2001
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 TGTTTCCTTTCTTTTTCATGTTTCTTGTGTCCTTACATTAATATCTGCACATCTGATGTA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 TAATITCTTTTCTTAGGGGTCTGTTACTGATGAATTATTATGTCCTTTTGGAGGTATCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 AGTIGACITITIGIAIACAACAIGCGAATITICCCITAAICCGGAGCIAITIGGIAAAA 544
Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic; neuroprotective; thrombolytic; osteopathic; antilnflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder; nervous system disorder; inflammation; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel foetal polypeptides encoded by polypuclectides comprising one of 477 sequences fully defined in the specification. The foetal polynuclectides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a full length cDNA which was assembled using expressed sequence tags (ESTs) found to be expressed in human foetal tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J, Arterburn MC,
Werhman T;
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antianaemic; dermatological; immunosuppressive; antiinflammatory;
  TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA TANKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           485 AGTIGACITITGIATACAACAIGCGAATITCCCITAAICCGGAGCIATICGIAIGAIAAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 THAGTAITITITGTCTGTAGTATCTATCCCAGCAATAGGTATATCCTGTTGCATCATAA 484
                                        nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system
                         Human; foetal protein; cytostatic; immunosuppressive; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel foetal polypeptides encoded by polypucleotides comprising one of 477 sequences fully defined in the specification. The foetal polypucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence was assembled using an expressed sequence tag (EST) found to be expressed in human foetal tissue cDNA libraries as the seed.
                                                                                                      nervous system disorder; inflammation; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                        J, Arterburn MC, Drmanac RA, Tang YT;
Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
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Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 316 BP; 61 A; 65 C; 50 G; 140 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 367-368; 715pp; English
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AAS30450 standard; DNA; 636 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  , Ford JE, Boyle BJ,
Asundi V, Zhou P, We
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15-SEP-2000; 2000US-0663870.
06-NOV-2000; 2000US-0707351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders and inflammation
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Best Local Similarity 53:8
Matches 70; Conservative
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P-PSDB; AAM06316.
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                                                                                                                                                                                     WO200155339-A2
                                                                                                                                                   Homo sapiens
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antiatrhitic; antirheumatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakata; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative; ds.
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2000US-0205515
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01-SEP-2000;
01-SEP-2000;
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24-FEB-2000;
02-MAR-2000;
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                                                                                                                                                                                                                                                                                                  Homo sapiens
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01-SEP-2000
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2000US-0251856

05-DEC-2000; 06-DEC-2000; 08-DEC-2000;

08-DEC-2000;

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2000US-0251988
             14 - SEP - 2000;

14 - SEP - 2000;

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14 - SEP - 2000;

21 - SEP - 2000;

25 - SEP - 2000;

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The invention relates to move a soluter prostact y quant related nuclear.

The invention relates to move a solute mon-bacterial prostatitis, chronic non-bacterial prostatitis, chronic non-bacterial prostatitis, chronic non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatitis, chronic non-bacterial prostatitis, prostaticis of prostaticis acute bacterial prostatitis, prostaticis of prostaticis, granulomatous prostatitis, malacoplakia, benign prostatic nyterizophy or hyperplasia, and prostate neoplasic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas, (1), (II) and antibody to (II) are useful for disorders in disorders (system disorders (paget's disease), autoimmune disorders (system clupus erythematosus, rheumatoid autoimmune disorders (system clupus erythematosus, rheumatoid carthritis), blood-related disorders (sickle cell anaemia), arthritis), blood-related disorders (sickle cell anaemia), comperioritis prostatis, musculoskeletal system disorders, neural activity and neurological disorders, uninary system disorders, neural activity and neurological disorders, inversal and disorders (all flammatory disorders (Alzheimer's disease and parkines), endocrine disorders (Alzheimer's disease) and patine disorders (solulary liver cirrhosis), condition and gali badder disorders disorders disorders disorders developmental and inherited disorders, disorders developmental and inherited disorders, disorders (page developmental and inherited disorders, disorders, disorders (page disorders) and wound healing and epithelial cell proliferation. (I) or (II) is useful to prevent skin aging, for preventing hair loss, to maintain
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                                                                                                                                                                                                                                                                                                                                                             Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel isolated prostate gland related nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; Score 34; DB 22; Length 636; 59.2%; Pred. No. 4.4; ative 0; Mismatches 40; Indels
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                                                             20000S-0251868.
20000S-0251869.
20000S-0251989.
20000S-0251990.
                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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Best Local Similarity 59.2
Matches 58; Conservative
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                                                                                     08-DEC-2000;
08-DEC-2000;
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Homo sapiens

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29-SEP-2000) 20000G-0236367.
29-SEP-2000) 20000G-0236367.
29-SEP-2000) 20000G-0236367.
29-SEP-2000) 20000G-0236369.
29-SEP-2000) 20000G-0236370.
02-OCT-2000) 20000G-0237039.
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13-OCT-2000) 20000G-023935.
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13-OCT-2000) 20000G-0241281.
20-OCT-2000) 20000G-0241808.
20-OCT-2000) 20000G-0241808.
20-OCT-2000) 20000G-0241809.
20-OCT-2000) 20000G-024677.
08-NOV-2000) 20000G-0246529.
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2000US-0235834
                                               17-JAN-2001; 2001WO-US01339
        WO200155320-A2
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2000US-0225758
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26-JUL-2000;
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                                                                                                                                                                                                                               573 TCTTGTGTTGCTCAGGCTGGTCTCAAACTCCTGCTAGCCTGTTGATTTTTGAGCCACTAA 514
                                                                                    The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence may be used to determine the number of NR genes per maize genome and to study the effect of various environmental conditions, incl. the presence of nitrate on the level of NR mRNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloned DNA sequence encoding maize nitrite reductase – useful for determn, of NR number and study of NR mRNA regulation and nitrate
                                                                Disclosure; SEQ ID NO 8918; 1297pp + Sequence Listing; English.
                                                                                                                                                                  Score 34; DB 22; Length 636;
Pred. No. 4.4;
0; Mismatches 40; Indels
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                                                                                                                                                 Sequence 636 BP; 153 A; 133 C; 129 G; 221 T; 0 other;
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                                                                                                                                                                                                                                                              Location/Qualifiers
9..1709
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59.2%;
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Best Local Similarity 59.2
Matches 58; Conservative
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Barash SC,
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                   WPI; 2001-465570/50
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 Rosen CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
maize plants grown under selected conditions. The CDNA is obted used to study NR mRNA regulation in maize. The CDNA is obtd. using lambda gill as the cloning vector and a spinach NR cDNA as heterologous probe. The CDNA clone (PCIB808) is 66% homologous at the nucleotide level with the spinach NR gene, however the maize DNA has a high G/C content (66.5%) as compared to that of the spinach gene (46%) and is 75% homologous at the amino acid level.
                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local Similarity 56.1%; Pred. No. 8.6;
Matches 64; Conservative 0; Mismatches
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14-AUG-2000;
18-AUG-2000;
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22-AUG-2000;
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33-AUG-2000;
01-SEP-2000;
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08-NOV-2000; 2000US-0246611.

08-NOV-2000; 2000US-0246613.

17-NOV-2000; 2000US-0249207.

17-NOV-2000; 2000US-0249209.

17-NOV-2000; 2000US-0249210.

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17-DEC-2000; 01-DEC-2000;                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC

Barash SC, Ruben SM; Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 20301; 3071pp + Sequence Listing; English.

amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic acitivity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the propose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-drived cells. AAK64703 concers and cancer human immune/haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK87694 represent invention. AAK84942 to AAK87690 and AAM82169 sequences trom the present invention. AAK84942 to AAK87690 and AAM82169

Sequence 16605 BP; 4009 A; 3696 C; 4212 G; 4688 T; 0 other;

°, Query Match 2.3%; Score 34; DB 22; Length 16605; Best Local Similarity 52.9%; Pred. No. 34; Matches 73; Conservative 0; Mismatches 65; Indels 0.

528 GCTAITCGTAIGATAAAAAAAGCTCTICCIGTICTGATICTTCTGGCGCTAICGGGGAGC 587

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14753 GATATAAATACAATAAAATTCACTCTTTCTATATACCATTTCCATGCTTTATGACAAGTG 14812
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648 CIGGATTIAACICCICG 665 | | | | | | | 1 | 1 14873 TITCCITAGCCACITCAG 14890 a

Search completed: June 18, 2003, 02:09:14 Job time : 270.397 secs

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M. capsulatus gene DNA encoding enzym Nucleotide sequenc R. marinus bacteri Mycobacterium tube Mycobacterium tube Pyrococcus abyssi Stealth virus nucl Pyrococcus abyssi Pyrococcus abyssi M. capsulatus gene	Bacillus lichenifo Human prostate exp Human prostate exp Human cytokine rec Human bone marrow Probe #8926 used t Human bone marrow Probe #8926 used t Human pluble Zalp M. cappulatus gene Human DNAX cytokin Gene encoding a su Human prostate exp Bacillus lichenifo S cerevisiae apopt DNA encoding novel Human prostate exp Stealth virus nucl Human nervous syst	Human immune/haema Human immune/haema Human secreted pro Human secreted pro Human immune/haema Human immune/haema Human immune/haema Human immune/haema Human immune/haema Human prostate exp Human Tryptophan-2 Gene #3348 used to Human prostate exp Human immune/haema Human immune/haema Human prostate exp Human immune/haema Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp	Granulocytic Ehrii Granulocytic Ehrii Granulocytic Ehrii Polyuuclectide seq Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp Human prostate exp
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: June 17, 2003, 13:22:38 ; Search time 198.603 Seconds (without alignments) 13391.616 Million cell updates/sec	Perfect score: US-09-674-277-2 Perfect score: 1181 Sequence: 1 ctgcaggagatggaaaaaaattttacttttttctctgcag 1181 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 2185239 seqs, 1125999159 residues Total number of hits satisfying chosen parameters: 4370478 Minimum DB seq length: 0 Maximum Match 0% Maximum Match 0% Maximum Match 10% Listing first 150 summaries	Database: N_Geneseq_101002:* SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:* SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1981.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1981.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1981.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1985.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1985.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1980.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1980.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1980.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1980.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1980.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1995.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1995.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA2001A.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA2001A.DAT:* SIDS2/gcgdata/geneseq-geneseqn-embl/NA2001B.DAT:* SIDS2/gcgda	Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

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The present sequence is specific to enterohemorrhagic Escherichia coliferior associated with the presence of virulence factors enterohemolysine (ehly) and intimin (eac). Nucleotides 237-570 also have 68% homology with the virK gene which codes for virulence proteins of Shigella flexneri. The present sequence is of plasmid origin. Fragments of the present sequence are used, as probes and primers, for detection of E. coli 0157:H7 and other enterohemorrhagic E. coli (EHEC), in human or animal samples, foods or the environment. The fragments are also useful for epidemiological studies. 181 GCCGTTATCTGTTGCATTTCCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCCG 240 301 AGCGTICCGGTCGGGATAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACCCCCA 360 1 CTGCAGGAGATGGAAAAAAAGCCAAAATAAAAAATTGCCCATCCCAGCGCGCTCCAGCTG Gaps Nucleic acid sequence specific to enterohemorrhagic Escherichia coli. Enterohemorrhagic Escherichia coli; EHEC; virulence factor; enterohemolysine; ehly; intimin; eae; virk gene; E. coli 0157:H7; ds New nucleic acid containing sequences specific to enterohemorrhagic Escherichia coli, particularly serotype 0157:H7, used for detecting these bacteria in food Query Match 100.0\$; Score 1181; DB 21; Length 1181; Best Local Similarity 100.0\$; Pred. No. 0; Matches 1181; Conservative 0; Mismatches 0; Indels 0; Sequence 1181 BP; 305 A; 317 C; 277 G; 282 T; 0 other; Frechon DTM, Laure FC, Thierry D; (SNFI) PASTEUR SANOFI DIAGNOSTICS. AAZ36102 standard; DNA; 1181 BP Claim 1; Fig 2; 48pp; French. 98FR-0005329 99WO-FR01000 11-FEB-2000 (first entry) WPI; 2000-013443/01. Escherichia coli. W09955908-A2. 27-APR-1999; 28-APR-1998; 04-NOV-1999. AAZ36102; RESULT 1 셤 ò g ద à ద a ò δ Qγ

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390 TGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGAC 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dysentery causing bacillus species can be rendered non-pathogenic delettion or mutefation of the virk and/or thyA genes. These non-pathogenic mutant strains can be used as attenuated vaccines to protect against infection with their wild type, disease causing
                                                                                                                                                                                                                  Highly safe attenuated live dysentery vaccine - prepd. from Shigella strain having mutated or deleted virk and/or thyA gene
                                                                                                                                                                                                                                                                                                                                                        13.5%; Score 159.4; DB 15; Length 1642; 65.1%; Pred. No. 1.1e-41;
                                                                                                                                                                                                                                                                                                                                    Sequence 1642 BP; 451 A; 311 C; 376 G; 504 T; 0 other;
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                                                       gene product.
                       Location/Qualifiers
373..1323
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                                TGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCAT
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AAQ55982/C
ID AAQ55982 standard; DNA; 1642
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Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.

Mycobacterium tuberculosis.

US6294328-B1

tuberculosis; strain H37Rv; strain CDC 1551;

Mycobacterium tuberculosis strain H37Rv genome SEQ ID

AA199683;

NO 2.

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Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5550 AACCTCAGGGATACCGCCAATGTTTGTTCCAATACAAGGCACTCCGCAAGCCATCGCTTC 6609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence, pAN240, is a plasmid carrying the B. subtilis PanBCD operon which encodes three enzymes of the pantothenate biosynthetic pathway (PanB. C and D). Pantothenate, also known as vitamin B5; is used as a nutritional supplement in mammals and humans. The invention concerns methods of producing recombinant microorganisms overexpressing at least one B. subtilis pantothenate blosynthetic enzyme. The microorganisms and methods of producing them are useful for producing a pantothenate or pantoate, which is a nutritional requirement for livestock and humans. The methods are also useful for the identification of pantothenate kinase modulators. Panto-compounds are produced at a significantly higher yield than prior art methods and can be produced independent of the need to feed precursors which decreases expense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 GCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAAT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 GACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTC 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant microorganism which overexpress a Bacillus subtilis pantothenate biosynthetic enzyme, useful for the high yield production of panto-compounds such as pantothenate and pantoate -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAGACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGCTCATTCC 571
                                                          PanBCD operon; pantothenate biosynthesis; cyclic; circular; pAN240; vitamin B5; nutritional supplement; panto-compound; pantoate; ds.
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                    Plasmid pAN240 carrying the B. subtilis PanBCD operon.
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54.4%; Pred. No. 1.2e-09;
Ive 0; Mismatches 108;
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Chimeric - Escherichia coli.
Chimeric - Bacillus subtilis.
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28-JUL-2000; 2000US-0221836.
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Matches 129; Conservative
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Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.

Venter JC;

White OR, Fraser CM,

WPI; 2001-647261/74. Fleischmann RD,

98US-0103840.

24-JUN-1998;

25-SEP-2001

(GENO-) INST GENOMIC RES

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2447493 CACCGTTCCGGCGCTCCGCCAGAATTGCCGGCATTACCGGCACGCCGGCGGGGGGG 2447552
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 AATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2447433 GGCGTCGGCCACCCGGTCCACCGACCTACCGTCGACCACTAGCCCAGTCTTGTTGTTGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 TTCTCTGGCGCTGCCTGCCATCATCCGGAGCGTTCCGGTCGGGATAAAAATCGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4403765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57.2; DB 22;
Pred. No. 8.3e-06;
0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCAGCCAGTACCATACCAAACGCTTCATTTTCC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.8%;
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Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                  monitoring.
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AAI99682 standard; DNA; 4411529

RESULT 5
AAI99682
ID AAI9

AAI99683 standard; DNA; 4403765 BP

RESULT 4
AAI99683
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ABK74404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TICICIGGCGCTGCCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 TGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 AATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGC
                                                                                                                                      Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.8%; Score 57.2; DB 22; Length 4411529; 54.2%; Pred. No. 8.3e-06; tive 0; Mismatches 98; Indels 0; G
                                                                                          Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC;
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                                                                                                                                                                                                                                                                                                                                                                                              98US-0103840
                                                                                                                                                                                                            Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White OR,
                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                                24 - JUN-1998;
                                           15-JAN-2002
                                                                                                                                                                                                                                                        JS6294328-B1
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AAI99682
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NAMES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
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ABK74404 standard; DNA; 1135 BP

RESULT 6 ABK74404/c

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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells; comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genewitzed from Bacillus cells to a substrate containing array of Bacillus celative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in which Bacillus cells adapt to changes in culture conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          follow up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring differential expression of several genes in first Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bacillus cells, by using substrate containing Bacillus genomic
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                                                                                                                                      Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                 Bacillus licheniformis genomic sequence tag (GST) #1695.
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27-MAR-2001; 2001US-279526P.
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13-AUG-2002 (first entry)
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Best Local Similarity 50.25
Matches 121; Conservative
                                                                                                                                                                                                                                                                                            Bacillus licheniformis
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                                                                                                                                                                                                                                                                                                                                                             WO200229113-A2.
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13-AUG-2002
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                                                                   Query Match
Best Local
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Once: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO
                           AAGCTITCCTICTCGGACAAAAGCAGCTITAAATCGCTGATGGCGTAAAGCTCTTCTACG 798
                                                                      actions of a second and a second several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag array
471 AACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCT
                                                     Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                          Bacillus clausii genomic sequence tag (GST) #1670.
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                                                                                                                                                                                                          ABK78827 standard; DNA; 783 BP
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27-MAR-2001; 2001US-279526P.
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                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berka R, Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                          Bacillus clausii.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200229113-A2.
                                                                                                                                        C 737
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                                                                                                                                                                                                                    413
                                                                                                                                                                                                                                                                     631 ITCCCAAGGGGGCATAAATAACCAGTTACTTCGTCTTCAACAACTTCCGGGATGCCACCA 572
                                                                                                                                                                                                                                                                                                                           114 GICICACIGGCGAIAACGGGCACGCCGGAGACIGACGCIICAGCCAGIACCAIACCAAAC 473
                                                                                                                                                                                                                                                                                                                                                                 474 GCTTCATTTTCCGAAGGCATGACCACCACCACTGGCAATCCGGTAGACGCTGGG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 TITIGGIIGCCIAGCAIAAGGACAICGIIIGICAAGCCGIITITCTICCACAAACIGCCIC 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 TCCCCCACGGGTAACAGCGTCCCTGTCAATTCTTCTGAATGACATCAGGGATCCCGCCC
                                                                                                                                                                Gaps
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                                                                                                       Length 783;
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                                                                                                                                                                Indels
                                                   Sequence 783 BP; 225 A; 149 C; 199 G; 208 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus clausii genomic sequence tag (GST) #1663.
                                                                                                       Score 48.6; DB 24;

·Pred. No. 3.8e-05;

0; Mismatches 124;
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ftp.wipo.int/pub/published_pct_sequences
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ID ABK78820 standard; DNA; 783 BP.
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27-MAR-2001; 2001US-279526P.
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                                                                                                                                                                Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R, Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                594 AGACGTG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 GCAATIG 385
                                                                                                                                         Similarity
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genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way on the magnet copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way can expression of genes or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is the method of the invention.

CC available. This sequence represents a genomic sequence tag (GST) used in the method of the invention.

CC specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 TCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGCCC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 TICCCAAGGGGGCATAAATAACCAGTTACTTCGTCTTCAACAACTTCCGGGATGCCACCA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 GTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAAC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573 ATTTTGTCGCGGTCACGTACCCCGCATGCCATCGCTTCAAGCGCCACTAAACCAAAG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%; Score 46.2; DB 24; Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus licheniformis genomic sequence tag (GST) #1771.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 783 BP; 224 A; 150 C; 204 G; 203 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.00024;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK74480 standard; DNA; 1227 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVOZYMES BIOTECH INC. (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 59.5
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 GCTTCATTTTC 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3erka R, Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-416684/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK74480;
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The invention describes a method of monitoring differential expression of genes in a first Bacilius cell relative to expression of the genes in other Bacilius cells, comprising hybridising labelled nucleic acid probes isolated from Bacilius cells to a substrate containing array of Bacilius gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacilius cells. The method is useful for monitoring global expression of several genes from a bacilius cell, discovering new genes, identifying possible functions of unknown open reading frames and continue copy in which Bacilius cells adapt to changes in culture conditions, in which Bacillus cells adapt to changes in culture conditions, control probes are one open reading frames in expression of genes may be used to provide a representation of the way continuental stress or other physiological provocation. Extensive collow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is the method of the invention.

Control of the invention.

Control of the invention.

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Control of the invention is electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 CATCCCCCACGGGTAACAGCGTCCCTGTCATTCTTCTGAATGACATCAGGGATCCCGC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 3.5%; Score 41.6; DB 24; Length 1227; Best Local Similarity 62.5%; Pred. No. 0.01; Matches 65; Conservative 0; Mismatches 39; Indels 0;
cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jonassen I, Jensen HB, Lien T;
Lsen JA, Fraser CM, Durkin AS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1227 BP; 368 A; 236 C; 300 G; 323 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :tp.wipo.int/pub/published_pct_sequences.
                                                         Claim 4; SEQ ID NO 1771; 200pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. capsulatus gene #67 for DNA array.
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ABQ90082 standard; DNA; 1098
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12-JAN-2001; 2001NO-0000239.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #0200255655-A2.
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Lillehaug JR,
Salzberg SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TIGR-) TIGR.
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"encodes AAY54077"

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22-APR-1998;
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The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression as as any of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                   334 CGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAA 393
                                                                                                                                                                                                                                                                                                   274 CTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAAATCGCGCAGTG 333
                                                                                                                                                                                                                                                                                                                                                                          943 cecceccaceccecceccarcecceerecarcarcarcarcarrerrerceccercecca 884
                                                                                                                                                                                                                                                                                                                                                                                                     394 TGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTT 453
                                                                                                                                                                                                                                                                                                                            1003 cccescccccrescccarsrcccccccasscccastccccaaccasccasccasccccars 944
                                                                                                                                                                                                                                                                                                                                                                                                                           824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exopolysaccharide; EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS5; EPS7; EPS8; EPS9; EPS10; EPS11; Lactobacillus helveticus strain LH59; activated D-galactose pyranose; saccharide; beta-qlycosyltransferase; undecaprenyl-phosphate-glycosyl-l-phosphate-transferase;
                                    Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-glycosyltransferase; EPS polymerase; glycosyltransferase; phosphofuranose; transporter; food; fermented milk product; yoghurt; cheese; flavour stability; organoleptic property; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONA encoding enzymes involved in exopolysaccharide biosynthesis.
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                                                                                                                                                                                                                                                  Score 40.8; DB 24; Length 1098; Pred. No. 0.018; Mismatches 117; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 CAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             823 GCAGCAGIGAGAIGCCCAGGCCIICGCGCAGGGCCGGAIGIACCACCA 776
                                                                                                                                                                                                                         Sequence 1098 BP; 156 A; 390 C; 374 G; 178 T; 0 other;
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                                                                                                 Claim 19; Page 81-82; 678pp; English
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/product= "EPS3"
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                                                                                                                                                                                                                                                                           0;
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus helveticus.
                                                                                                                                                                                                                                                                 Best Local Similarity 48.7
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-
              WPI; 2002-557818/59
                                                                            capsulatus genes
                                                                                                                                                                                                       invention.
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                                                                                                                                                                                                                                                      Query Match
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The present sequence encodes enzymes involved in the biosynthesis of exopolysaccharides (EPS). These enzymes are designated EPS1-EPS11. and are encoded by open reading frames eps1. The enzymes are isolated for the objoint reading frames eps1. The proteins are used from Lactobacillus helveticus strain LH59. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hami-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the end of a chain of sugar residues bonded to the unit, present at the end of a chain of sugar residues bonded to the phosphate-transferase; EPS2, EPS3 and EPS4 are alpha-
phosphate-transferases; EPS5 and EPS6 have homology with a beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY54075; AAY54076, AAY54077, AAY54078, AAY54079, AAY54080,
AAY54081; AAY54082, AAX54083, AAY54084; AAX54085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /hote-"encodes AAY54085; contains 1 stop codon at nucleotides 12867-12869"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           new recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties fermented milk products
                                                                                                                                                                                                 "encodes AAY54079"
                                                                                                                                                                                                                                                                                                               /note= "encodes AAY54080'
7095..8258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "encodes AAY54082"
135..10253
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                                                                                      "encodes AAY54078
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product= "EPS7"
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                                                        "EPS4
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11664..13181
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'98EP-0201312.
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6098..7090
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products
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    2762 TAACTAAAGAAGATCTCAAATCAGGTTGTTTAAATAGTTTATCGACTGCATCTGCTGCTT 2703
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glycosyltransferase; EPS7 has homlogy with an EPS polymerase; EPS8 is a glycosyltransferase, EPS9 catalyses the transfer of phosphofuranose onto the following repetitive unit; EPS10 transports the polysaccharides formed; and EPS11 is involved in the synthesis and export of formed polysaccharides. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
                                                                                                                                               226 CAATGATCTGTGCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGG
                                                                                                                                                                                         286 CTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATG
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                                                                                                                                                                                                                                                                           TCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCA
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eps operon; Lactobacillus helveticus LH59; enzyme; eps1; eps2; eps3; eps4; eps5; eps6; eps7; eps8; eps9; eps10; eps11; expolysaccharide blosynthes19; Eps5; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product- "eps3"
/note- "encodes AAX43779; this CDS is specifically
claimed (claim 11)"
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/product= "eps4"
/note= "encodes AAY43780; this CDS is specifcally
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  claimed (claim 11)"
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                                                                                                      Query Match 3.4%; Score 40.6; DB 21; Length 14245; Best Local Similarity 46.3%; Pred. No. 0.093; Matches 133; Conservative 0; Mismatches 154; Indels 0;
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                  466 TACCAAACGCTTCATTTTCCGAAGGCATGACCACCACCACTGGCAATC 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide seguence of the eps operon of L. helveticus LH59.
                                                                                  Sequence 14245 BP; 5095 A; 1755 C; 2545 G; 4850 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                            AA230356 standard; DNA; 14245 BP
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The present sequence represents the eps operon of Lactobacillus helveticus LH59. The operon contains 11 open reading frames, and encodes enzymes (eps1. eps2, eps1, eps4, eps5, eps6, eps7, eps8, eps9 and eps11) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse the formation of specific intersugar bonds forming a bond (in alpha or beta anomeric form) between Cl, carrying the reducing aldehyde group of an activated D-Galp (galactose in pyranose form), and a phosphate group on a lipophilic or proteinaceous primer. The enzymes are used to produce EPS that have antitumor or problotic properties or are used in foodstuffs to improve organoleptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or problotic properties or useful in fermented milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encodes AAY43787; the sequence contains 1 stop codon at nucleotides 12867-12869; this CDS is specifically claimed (claim 11)"
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AAX43783, AAX43784, AAX43785, AAX43786, AAX43787.
                                                                                                        claimed (claim 11)"
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                                                                                                                                                                                                                                                       /note= "encodes AAY43782; this CDS is specifcally claimed (claim 11)"
                                                                                                                                                                                                                                                                                                                                                                           encoues AAY43783; this CDS is specifically claimed (claim 11)"
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    claimed (claim 11)"
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claimed (claim 11)"..6095
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product= "eps5"
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/product= "eps7"
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certings (e.g. proteases and lippases used in washing powder, hydrolytic enzymes used in bleaching). The isolated nucleic acid molecules and vectors are useful in the manufacture of encoded polypeptide, as probes cor isolating homologous sequences (e.g. from other bacteriophage species), as well as for detecting the presence of the bacteriophage a culture of host cells. The polypeptides can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns. Because the host organism of the RM378 bacteriophage is a thermophile, the enzymes and proteins of the RM378 bacteriophage are significantly more thermostable than those of other (e.g. mesophilic) bacteriophages, such as the T4 bacteriophage of Escherichia coli. The enhanced stability of the enzymes and proteins of RM378 bacteriophage and allows their use under temperature conditions which would be prohibitive for other enzymes, thus increasing the range of conditions which can be employed not only in DNA research but also in commercial settings.

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producing thermophilic enzymes useful in DNA research and commercial

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398 ATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGC 457

Sequence 130480 BP; 37304 A; 27752 C; 27687 G; 37737 T; 0 other;

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Gaps

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44; Indels

0.34;

3.4%; Score 40.6; D. Local Similarity 60.4%; Pred. No. 0.34 les 67; Conservative 0; Mismatches

Query Match Best Loc Matches

DB 22; Length 130480;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 TCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCA 465
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qualities and flavour. When expressed by lactic acid bacteria, EPS imple free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or cheese).
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                                                                                                                        Length 14245;
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                                                                                 Sequence 14245 BP; 5095 A; 1755 C; 2545 G; 4850 T; 0 other;
                                                                                                                                                                   Indels
                                                                                                                      Score 40.6; DB 21;
Pred. No. 0.093;
0; Mismatches 154;
                                                                                                                          3.48;
                                                                                                                                                Local Similarity 46.3
nes 133; Conservative
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Genome; thermophilic enzyme; washing powder; bleaching; ds
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                                                     R. marinus bacteriophage RM387 genomic DNA.
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           AAF25833 standard; DNA; 130480 BP
                                                                                                                                        99US-0137120
                                                                                                                                                     (DECO-) DECODE GENETICS EHF.
                                                                                                                          02-JUN-2000; 2000WO-IB00893
                                        (first entry)
                                                                                 Rhodothermus marinus.
                                                                                                                                                                         Kristjansson JK;
                                                                                              WO200075335-A2.
                                                                                                                                        02-JUN-1999;
                                        12-APR-2001
                                                                                                            14-DEC-2000.
                          AAF25833;
     AAF25833
RESULT
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the tat correspond to positions that differ in the
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This invention describes a novel isolated nucleic molecule (I) comprising the genome of bacteriophage RM 378. The invention also describes (1) an isolated nucleic acid which encodes a polypeptide obtainable from bacteriophage RM 378 or its active derivative or fragment; (2) an isolated bacteriophage RM 378 (II); (3) a DNA construct (III) comprising operatively linked to a regulatory sequence; (4) a host cell comprising (III); and (5) an isolated polypeptide (IV) obtainable from (II), its active derivative or fragment. Bacteriophage RM 378 is useful for

Isolated nucleic acid from bacteriophage RM 378 encoding enzymes useful in recombinant DNA technology -

WPI; 2001-061727/07.

Claim 3; Fig 1A-1Q2; 138pp; English.

Aevarsson A;

Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds. 458 CAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGC 508 Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2. AAI99683 standard; DNA; 4403765 BP. 98US-0103840. 98US-0103840 Mycobacterium tuberculosis. (first entry) US6294328-B1. 15-JAN-2002 24-JUN-1998; 24-JUN-1998; 25-SEP-2001. AA199683; RESULT 14 AAI99683,

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nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic monitoring. Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID-6294328B1.
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Querellou J,
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nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                            453 TCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATC 512
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                                                                                                                                                                                                                                                                                   393 ATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCT 452
                                                                                                                                 Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                         monitoring.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the first strain at lositions in the complete sequence of the first strain at lositions in the complete sequence of the genome that correspond to positions that differ in the
                                                                                                                                                                                                                                                                                                   577929 ACGCGAGGCAGCCGCCCCACGCGGGCCACCGGTGTGCCGCACGCTTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                Gaps
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                                                                                                                                                                 DB 22; Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
                                                                                                                                                                                            92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC;
                                                                                                                                                              3.4%; Score 39.8; DE 50.8%; Pred. No. 4.8; Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA199682 standard; DNA; 4411529 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
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                                                                                                                                                                                             95; Conservative
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Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                         333 GCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGA
                                                                                                                                                                                                                                 393 ATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCT
                                                                                                                                                                                                                                                                                         453 TCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATC
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                                            DB 22; Length 4411529;
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\/-tag = Annis sequence overlaps with the 3'
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                                        Score 39.8; DB 22; Length
Pred. No. 4.8;
0; Mismatches 92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus abyssi genomic fragment #6.
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(IFRE-) IFREMER INST FR RECH EXPL MER
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                                          3.4%;
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                                    Query Match
Best Local Similarity 50.8
Matches 95; Conservative
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abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41226. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to NAFP. The contract of the present invention have the proteins of the proteins are stable at very high temperatures, some up to NAFP. The contract of the proteins are stable at very high temperatures.
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                                                                                                as WO200065062, which
                                                                                                                                                              Length 265118;
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AAH75903-AAH75920 and AAG66436.
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                                                                                                                                                                                                                                        3.3%; Score 39.2; DB 20;
1larity 14.5%; Pred. No. 0.15;
Conservative 138; Mismatches 146;
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misc_difference 3750
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The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression as agenomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ARQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 CGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACAT 384
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                                                                                                                                                                                                                                     Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus capsulatus genes
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                                                                                                                                                                                                             DNA array useful for determining differential expression of
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Pred. No. 0.11;
0; Mismatches 91; Indels 0;
                       HB, Lien T
Durkin AS;
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                          Eidhammer I, Jonassen I, Jensen
Lossius I, Eisen JA, Fraser CM,
                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 135-136; 678pp; English.
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Best Local Similarity 50.5%;
Matches 93; Conservative
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                          Birkeland NK,
Lillehaug JR,
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27-MAR-2001;
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                                                               Lillehaug JR
Salzberg SL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abysi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal worts. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAM41225 and the 3' end of this sequence overlaps with the 5' end of AAM41227. The proteins of the present invention have various potential industrial uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 GCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                since the proteins are stable at very high temperatures, some up to 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 ATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCT
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Note: This patent is in the same patent family as WO200065062, which
contains additional sequences as shown in AAB99132-AAB99143,
AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the genomic sequence of Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 349980 BP; 98084 A; 80447 C; 77665 G; 93784 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                            New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
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Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.2; DB 22;
Pred. No. 1.7;
0; Mismatches 68;
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(TIGR-) TIGR.
                                                                                             (CNRS ) CNRS CENT NAT RECH SCI;
(IFRE-) IFREMER INST FR RECH EXPL MER
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 511-606; 1657pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%;
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12-JAN-2001; 2001NO-0000239
                             99FR-0005034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Conservative
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                                                                                                                                                                                                                                                                                       WPI; 2001-126236/14.
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                                                                                                                                                                                      Forterre P,
Querellou J,
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                                 21-APR-1999;
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ABQ901897
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20-FEB-2001; 2001WO-US05171
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     NAME OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                        The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in coher Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus close described by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells. The method is useful for monitoring new genes in one or more second Bacillus cells. The method is useful for monitoring genes or more second Bacillus cells. The method is useful for monitoring new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive equals one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACCACTG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTGTATAAAATCTTTCAGGCCGCCGGAGTCTGCCCCGATAACAGGCGTCCCGCAGGCG 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 AGCGCTTCAAGGGCGGAATTTCCGAAGGTTTCCGTCGGAGAAGGAAAGACGAACAAATCT 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                               Monitoring differential expression of several genes in first Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                        cell relative to expression of same genes in one or more second
Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 24; Length 1108; Pred. No. 0.33; 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1108 BP; 304 A; 290 C; 246 G; 268 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate expression marker cDNA 47255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                     Claim 4; SEQ ID NO 1730; 200pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.18;
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Best Local Similarity 54....
And 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 GCAATCCGGTAGA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | || || GAGCTCGCATAGA 794
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pharmacogenomic marker;
                                                                                                                                                                     sequenced tag array
                                               WPI; 2002-416684/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200160860-A2
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Berka R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
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셤
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 CAATICGCCCTAIAGIGAGICGIATIACGCGCGCTCACIGGCCGTCGTITIACAACGICG 376

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCAGGAGATGGAAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human soluble Zalphall cytokine receptor cDNA degenerate sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 386 BP; 110 A; 97 C; 93 G; 85 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.24;
0; Mismatches
                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 9300; 11750pp; English
                                                                                                                                                                                                                                                                                                        Monahan JE;
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                                  2000US-189862P.
2000US-207454P.
                                                                                                      2000US-211314P.
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                                                                                                                                                                      2000US-255281P
      2000US-183319P
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Best Local Similarity 56.19
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                     Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-662795/76.
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17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
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Homo sapiens

18-OCT-2001

Sprecher CA,

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1063 CGATAATCCGTCGAAGTCTGAGGATGGAAGGAAGGTGAAGGCTGTTCCTGAAAGGAATAA 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 GIGAGAIAGGCACAACAAIGAAAICACACAGAIAAIICAGGGAAAACGIICIGGICIIAC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GTGGAAYTINCAYCCNWSNACNTINACNTHACNTGGCARGAYCARTAYGARGARYTNAA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       943 GGGTGATGTAGGTTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 RGAYGARGCNACNWSNTGYWSNTHNCAYMGNWSNGCNCAYAAYGCNACNCAYGCNACNTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid encoding zalphail polypeptide, useful for treating e.g. viral infection or tumors, and for identifying ligands that stimulate cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a degenerate DNA sequence that encompasses all DNAs encoding zalphall (see AAY79312), a novel human class I cytokine receptor that may be involved in an apoptotic cellular pathway, or is a cell-cell signalling molecule, growth factor receptor, or extracellular matrix associated protein with growth factor hormone activity. The degenerate sequence serves as a template for optimizing expression of polynucleotides in various cell types and hosts. The invention provides zalphall polypeptides, polynucleotides (see also AAZ94533), agonists, annagonists and antibodies, and methods for their use in the treatment and diagnosis of conditions associated with altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%; Score 36.6; DB 21; Length 1614; 30.7%; Pred. No. 0.55; ive 35; Mismatches 132; Indels 0;
                                                                  Cytokine receptor; zalphall; human; chromosome 16pl1.1; apoptosis; signal transduction; growth factor; cancer; tumour; infection; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1614 BP; 209 A; 190 C; 302 G; 204 T; 709 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conklin DC, Novak JE, Hammond AK;
                                   Human cytokine receptor zalphall degenerate DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2(a); Page 150-151; 190pp; English.
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zalphall expression or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0159254.
99US-0265117.
99US-0347930.
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/*tag= a
58..1614
/*tag= b
18-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-292825/25.
P-PSDB; AAY79312.
                                                                                                                                                                                                                                                                                                                               WO200017235-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                  33-SEP-1999;
                                                                                                                                                                  Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1998;
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06-JUL-1999;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated soluble zalphall cytokine receptor inhibiting or antigonising the ligand activity-induced proliferation of nantipoliting or antigonising the ligand activity-induced proliferation of haematopoletic cells and haematopoletic cell progenitors preferably calpha is useful for treating immune and inflammatory disorders, for reducing proliferation of neoplastic B or T cells, for suppressing an immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus (SLE) and dlabetes; espis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble Zalphall cytokine receptor CDNA degenerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1063 CGATAATCCGTCGAAGTCTGAGGATGGAAGGAAGGTGAAGGCTGTTCCTGAAAGGAATAA 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 NGAYCARWSNGGNAAYTAYWSNCARGARTGYGGNWSNTTYYTNYTNGCNGARWSNATHAA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       943 GGGTGATGTAGGTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   883 GTGAGATAGGCACAACAATGAAATCACACAGATAATTCAGGGAAAAACGTTCTGGTCTTAC
                                                                                                                                                                                                                                                                          Nelson AJ;
                                                                                                                                                                                                                                                                                                                                                         Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune
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                                                                                                                                                                                                                                                                          Holly RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132;
                                                                                                                                                                                                                                                                          Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 179; 243pp; English.
                                                                                                                                                                                                                                                                            West JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ94534 standard; DNA; 1614 BP
                                                                                                                                                                       05-APR-2000; 2000US-194731P. 28-JUL-2000; 2000US-222121P.
                                                                                                                                 03-APR-2001; 2001WO-US10872
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                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                              Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                             response in a mammal
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Query Match Best Local Si Matches 74;

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AAZ94534;

AAZ94534 ID AAZ9 XX AC AAZ9

RESULT 23

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AAK34523 standard; DNA; 598 BP.
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30-JUN-2000;
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                                                                                                                        06-NOV-2001
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                                                                                   AAK34523;
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  RESULT 25
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                        AAK34523
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                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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Pred. No. 0.42;
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                                                                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #8663.
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                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.18;
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2000US-0207456.
2000US-0608408.
                                                                                                                                         ABA60358 standard; DNA; 598
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2000US-0236359.
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                                                                                                                                                                                                                               (first entry)
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nes 68; Conservative
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1123 A 1123
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                                     357 R 357
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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30-JUN-2000;
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                                                                                                                                                                                   ABA60358;
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                                                                                                                        ABA60358,
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1113 AAAGGAATAAAAGTGACATCATGCCCTCTTTTTCTGGCTTCCGGAGCAATTTTACTTTT 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503 TAAAATGTACAGGCCACTTGTACAGAGCTCATGATGACAGTGAATTGAACACTCATTGTC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                        Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
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0
                                            Human bone marrow expressed single exon probe SEQ ID NO: 9080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.2; DB Pred. No. 0.42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR;
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2000US-0608408.
2000US-0632366.
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2000US-0236359
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(first entry)
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Matches 68; Conservative
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI40240;
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1133 A 1133
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                                                                                                WO200177171-A2
                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                           Sprecher CA,
                                                                                                                                             18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
Matches 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1113 AAAGGAATAAAAGTGACATCATGCCCTCTTTTTCTGGCTTCCGGAGCAATTTTACTTTT 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1053 TTAMATTCCCCGATAMTCCGTCGAAGTCTGAGGATGGAAGGAAGGTGAAGGCTGTTCCTG 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 TAAAATGTACAGGCCACTTGTACAGAGCTCATGATGACAGTGAATTGAACACTCATTGTC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic; inflammatory disorder; haemostatic; cell proliferation; immune disorder; autoimmune disease; rheumatoid arthritis; multiple solerosis; cancer; myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for prodicting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                        to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human soluble Zalphall cytokine receptor variant degenerate cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.2; DB 22; Length 598; Pred. No. 0.42; 0; Mismatches 53; Indels 0
                                                                                   microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 598 BP; 169 A; 109 C; 137 G; 183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID No 8926; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD22970 standard; cDNA; 741 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1%;
                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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                                                                                                         genetic disorder; ss
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Best Local Similarity
Matches 68; Conserv
                                          used
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                                                                                                                                                                                             WO200157272-A2
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
30-JUN-2000;
                                          Probe #8926
                                                                                                                                                                                                                                     09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                     Probe;
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The invention relates to an isolated soluble zalphall cytokine receptor polypeptide and their cDNA molecules. Zalpha proteins are useful for inhibiting or antagonising the ligand activity induced proliferation of heematopoietic cells and haematopoietic cell progenitors preferably imphoid cells which are natural killer cells or cytotoxic T cells. Zalpha is useful for treating immune and inflammatory disorders, for reducing proliferation of neoplastic B or T cells, for suppressing an immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune requiation including autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus (SIE) and diabetes; sathum, ulocarative colitis, inflammatory bowel disease, copinis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble Zalphall cytokine receptor variant cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1073 TCGAAGTCTGAGGATGGAAGGAAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACATC 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || | | : | : |:||: | | 319 GGNAAYTAYWTUGARWSNMGNCARTAYAAYAH 438
ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 ACNWSNTGYWSNYTNCAYMGNWSNGCNCAYAAYGCNACNCAYGCNACNTAYACNTGYCAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       833 AACCGTTACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGGTGAGATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  893 CACAACAATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        953 GGTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holly RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 222-223; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              West JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000US-194731P. 28-JUL-2000; 2000US-222121P.
                                            viral infection; variant; ss
                                                                                                                                                                                                                                                                                                                                                         03-APR-2001; 2001WO-US10872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response in a mammal
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AAD06409 standard; DNA; 1704 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel DNA array giving a representation of a mumber of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 CTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAGTG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   952 cccreccecerereccarracececererecceseresecereseces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 CGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 TGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCCTCCCGGCAGCCGGGCACGTCGTGACGATGCCCCGCGTGCAGGCGGCGGCTT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus capsulatus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel DNA array useful for determining differential expression of
                                                                                                                                                        Micro array; gene; ds; differential expression; gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36.2; DB 24; Length 1029;
Pred. No. 0.58;
0; Mismatches 123; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                            Jonassen I, Jensen HB, Lien T
Eisen JA, Fraser CM, Durkin AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1029 BP; 159 A; 359 C; 353 G; 158 T; 0 other;
                                                                                                                           M. capsulatus gene #191 for DNA array.
                                                                                                                                                                                                                                                                                                                                                (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN
(TIGR-) TIGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 144; 678pp; English.
                              0206/c
ABQ90206 standard; DNA; 1029 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.18;
                                                                                                                                                                                                                                                                         14-JAN-2002; 2002WO-NO00019.
                                                                                                                                                                                                                                                                                                                                                                                              Eidhammer I,
                                                                                                                                                                                                                                                                                                     12-JAN-2001; 2001NO-0000235.
                                                                                                                                                                                                                                                                                                                                                                                                           Lossius I,
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 47.2
110; Conservative
                                                                                                                                                                                     Methylococcus capsulatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PI; 2002-557818/59.
                                                                                                                                                                                                                 WO200255655-A2.
                                                                                                                                                                                                                                                                                                                                                                                           Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                                                                                       Salzberg SL;
                                                                                                01-0CT-2002
                                                                                                                                                                                                                                              8-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nvention
                                                                     ABQ90206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
             RESULT 28
                            ABQ90206,
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The present sequence is named by contine treeperson and the present sequences translational DNAD. DCRS3 gene is located on the present sequences translational DNAD. DCRS3 gene is located on the promosome lepi2. Cytokine receptors, fragments and antibodies are useful for treating immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are useful in drug screening to identify compounds having binding affinity to the receptor subunit. Modulators of DCRS are useful compulating the physiology or development of a cell or tissue culture cells. A purified DCRS is useful as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to production of antibody to the endogenous receptor. Cytokine receptor sequences are useful as probes of detecting a levels of the cytokine receptor in patients suspected of having an immunological disorder. Antibodies have therapeutic value, are useful as potent antagonist, in detecting or quantifying ligands, for isolating DCRS proteins and peptides, to screen expression libraries for particular expression products, to raise anti-idiotypic antibodies and for detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACNWSNTGYWSNYTNCAYMGNWSNGCNCAYAAYGCNACNCAYGCNACNTAYACNTGYCAY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   893 CACAACAATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : | : | : | | : | : | ANYTHIACHTGGATHYTHWSNAAYAATACHGGYTGYTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 ATHAARGAYMGNACNYTNGAYYTNMGNCARGAYCARTAYGARGARYTNAARGAYGARGCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mammalian receptor proteins related to cytokine receptors, useful for regulating cell development and for diagnosis and treatment of
                                                                                                                                                                                                                       Human; immunomodulator; DNAX cytokine receptor subunit 3.1; DCRS3.1; therapy; immunological disorder; drug screening; cell development;
                                                                                                                                                      Human DNAX cytokine receptor subunit 3.1 reverse translational DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is human DNAX cytokine receptor subunit 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1704 BP; 227 A; 201 C; 315 G; 209 T; 752 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 17-18; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0443060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-2000; 2000WO-US31363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.68;
                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-343800/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                             chromosome 16pl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200136467-A2.
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-1999;
                                                                     10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorman DM;
AAD06409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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1013 ATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCG 1072

RESULT 29 AAD06409

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9780 RCSRDSTYSSRGYDANSTSRYSSRYSSRYSSDSTYSAKYCAKSTTBTBCYYDAYDACYDA 9721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                       cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                 478 CATTITICCGAAGGCATGACCACCACCACTGGCAATCCGGTAGACCGGTAACGCTGGGAAAA
       418 CACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 3338.
                                                                                                                                                                                       9720 YDANCYSSDSTYTBYCSRRCCC 9699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 609; 11750pp; English.
                                                                                                                                                                        619
                                                                                                                                                                           GIGCIICGIAIICIICACGCCC
                                                                                                                                                                                                                                                                      ABV03347 standard; cDNA; 650 BP
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2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-183319P
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                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (c) assessing the ef
cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate
pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000; 2
16-MAR-2000; 2
25-MAY-2000; 2
09-JUN-2000; 2
18-JUL-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                             13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2001
                                                                                                                    538
                                                                                                                                                                          598
                                                                                                                                                                                                                                                                                                 ABV03347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits of cellulose synthesic equipment, that can be used to increase the amount of cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCGCCGTTATCTGTTGCATTTCCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357
298 GGAAGCGTTCCGGTCGGGATAAAAATCGCGCCAGTGCGCCGGTCCATGCAGACACATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1073 TCGAAGTCTGAGGATGGAAGGAAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 10732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
                                                                                                                                                                                                                                                                                                   Cellulose synthase; cellulose production; increase yield; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A gene encoding a cellulose synthetic equipment - for in the amount of cellulose synthesised in a plant body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 36.2; DB 21;
L Similarity 15.4%; Pred. No. 2.3;
68; Conservative 174; Mismatches 197;
                                                                                                                                                                                                                                                                         Gene encoding a subunit of cellulose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 14-21; 32pp; Japanese
                                                                                                                                                                                )594/c
AAA10594 standard; DNA; 10732 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0239998
                                                                                                                                                                                                                                                                                                                                                                                                               98JP-0239998
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MIZU/) MIZUNO K.
(OJIP ) OJI PAPER CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-342371/30.
P-PSDB; AAY85179.
                                                                                             1133 A 1133
                                                                                                                                                                                                                                                                                                                                 Vigna angularis
                                                                                                                                                                                                                                                                                                                                                           JP2000060568-A.
                                                                                                                       W 499
                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-AUG-1998;
                                                                                                                                                                                                                                               29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                     29-FEB-2000.
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Best Local S
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                                                                                                                                                                                                                    AAA10594;
                                                                   439
                                                                                                                       499
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Matches
                                                                                                                                                                              AAA10594
                                                                                                                                                                 RESULT
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WO200102550-A2.
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Nelissen BJM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2001
                                                                                                                                                                 Best Local Sim
Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH29949;
                                                                                                                                                      Query Match
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                                                               ö
                                                                                                   NGTIATTAATTAAAATTTNNTTCCCCCCCCCATTNTTAACCAAATNCCCTTTTCCAT 598
                                                                                                                                     74 TCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAATGTGATAAATTACTC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                     14 AAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAGTAGGCCTGT
                                                               Gaps
                                                               ö
                                   Score 36; DB 23; Length 650;
Pred. No. 0.51;
                                                            76; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Differential gene expression; genomic sequenced tag; GST;
                                                                                                                                                                                                                                                                                                                                                       Bacillus licheniformis genomic sequence tag (GST) #757
          Sequence 650 BP; 180 A; 110 C; 118 G; 199 T; 43 other;
                                                                                                                                                                                                                                                                                                                                                                                             altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                       CGTTACCGGAAAACCGCTGAACAAAATTCGG 164
                                                                                                                                                                                                        GGTTAATTTTAAACCAATTAANAAAAAGGG 629
                                               Pred. No. 0.51
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 757; 200pp; English.
                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVOZYMES BIOTECH INC.
                                                                                                                                                                                                                                                               ABK73466/c
ID ABK73466 standard; DNA; 1427
                                   ch
1 Similarity 49.7%;
75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-0CT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2001; 2001WO-US31437.
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berka R, Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequenced tag array
                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            40200229113-A2.
                                                                                                                                                                                                                                                                                                                              13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2002.
                                                                                                                                                                                       134
                                   Query Match
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                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 GACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGCTCATTCCCAGGTG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 ATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              975 CTCCATGTCTTCTTCAA---ACAGTTCATGCAATACCCGCTTGATCAAATCGAAGCC 919
                                                                       13
13
                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
environmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information available. This sequence represents a genomic sequence tag (GST) used the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast and fungal nucleic acids encoding proteins involved in a pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 CAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 TTCTGTCTGCTGACGCAGACGTGCTTCGTATTCTTCACGCCCCGGCGCCCACCACGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1035 ATGCTCCATATAGCGGAAGTAATTTTCAAATTCCGCTTCTCCGGTTCCTAAAACGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGAAATGATTTCCCTTCCATCTTCAGCTGATACAATACAGCAGCAGCATAAATTCATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITITICGGGACGIAGCAICCCCACCIGAACGAIAAGCGGAACAIIGIC 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918 TITITGCTTCGTCAGCCTTGCCACCATGCTGATGAGCGGAATGTCTTC 871
                                                                                                                                                                                                                                                                                                                                                                             3.0%; Score 36; DB 24; Length 1427; 6.0%; Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast; fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S cerevisiae apoptosis associated coding sequence YKR040C.
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malcorps IKL;
                                                                                                                                                                                                                                                                                                               Sequence 1427 BP; 378 A; 305 C; 379 G; 365 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luyten WHML,
                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH29949 standard; DNA; 1859 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Backer MD,
Reekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-2000; 2000WO-BE00077.
                                                                                                                                                                                                                                                                                                                                                                                                              46.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-367042/38.
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAG70913
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                                                                                       The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemta and neurodegeneration. The present sequence is one of the S. cerevisiae coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                           programmed cell death, useful for treating proliferative yeast and fungal infections, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                              ACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGG 490
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                          Score 36; DB 22; Length 1859;
Pred. No. 0.95;
0; Mismatches 50; Indels (
                                                                                                                                                                                                                               Sequence 1859 BP; 663 A; 297 C; 358 G; 541 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 1097; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS65293 standard; cDNA; 426 BP
                                                               Claim 1; Fig 1; 218pp; English.
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Local Similarity 56.9%;
nes 66; Conservative C
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23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                    disorders, yeast
certain diseases
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Matches
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AAS65293/
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to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics forensics, gene mapping, identification of mutations capposable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human cold sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                           525 AACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGCTCATTCCCAGGTGTTCTGTC 584
                                                                                                                                                                                                                                                                                                                                                                              cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                           Length 426;
                                                                                                                                                                                                                                                                                                                           27; Indels
                                                                                                                                                                                                                                                              Sequence 426 BP; 113 A; 105 C; 113 G; 95 T; 0 other;
                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 48863.
                                                                                                                                                                                                                                                                                             3.0%; Score 35.8; Di
65.8%; Pred. No. 0.47
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 9567; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| | |||| |||||
334 CTCTGGGGAAGACTGGCTT 316
                                                                                                                                                                                                                                                                                                                                                                                                                             585 TGCTGACGCAGACGTGCTT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV48872 standard; cDNA; 488 BP.
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20000S-207454P.
20000S-211314P.
20000S-219007P.
20000S-255281P.
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nes 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate
pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-2000; 2
25-MAY-2000; 2
09-JUN-2000; 2
18-JUL-2000; 2
13-DEC-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2001.
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                                                                                                                                                                                                                                                                                                  Query Match
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specification or its complement. (I) is useful for:
(a) assessing whether a patient is affilicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer (f) assessing the prostate cell carcinogenic potential of a compound:
(g) determining whether prostate cancer has meracine.
(h) assessing the accreance.
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   /*tag* d
   /*tag* d
   /note* "this nucleotide is represented as a * in the
   specification, and is included to maintain the
   base numbering given in the specification"
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ntain the
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                                                                                                                                                                                                                                      5 AGGAGATGGAAAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAG
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                                                                                                                                                      (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                            3.0%; Score 35.8; DB 23; Length 488; 6.3%; Pred. No. 0.51; ve 0; Mismatches 52; Indels 0
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                                                                                                                                                                          Sequence 488 BP; 170 A; 107 C; 100 G; 111 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Stealth virus nucleic acid clone, SEQ ID NO: 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Stealth virus; detection; diagnosis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      BP
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/note= "this
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                                                                                                                                                                                                                                                                                                                                                     AAX84332 standard; DNA; 5059
                                                                                                                                                                                                      Similarity 56.3%;
67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stealth virus.
                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-1999
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                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                         Local
                                                                                                                                                                                                                 Matches
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specification, and is included to maintain the
base numbering given in the specification*
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specification, and is included to maintain the
base numbering given in the specification"
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specification, and is included to maintain the
base numbering given in the specification"
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**This nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification**
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specification, and is included to maintain the
base numbering given in the specification"
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FT misc_difference 3857 FT /*tag= a) represented as a * in the specification, and is included to maintain the performance of the specification in the specification. FT misc_difference 3860 has numbering given in the specification. /*tag= al /*t	Query Match 3.0%; Score 35.8; DB 20; Length 5059; Best Local Similarity 14.7%; Pred. No. 2; Matches 98; Conservative 235; Mismatches 327; Indels 5; Gaps 1; Qy 516 TAGACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACTCCCGCTCATTCCCAGG 575	Db 2990 THGNEDGDWXYSNGDARNTRVHANSYYANYWBKGDSNCYCNHGNAYKSVTAKTNSVNTGS 2931 QY 636 CAGCGAAATTCCCTTCCATCTTCAGCTGAATACAACGCAGCATAAATTCATGT 695 :: :: :: :: :: :: :: Db 2930 TNCYDAAHDGATKATDAHNYWSNGKTYKNCBKGDDADCYDAHAVYASHRTKYNANYWSGN 2871 QY 696 CCTTTTCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAACATTGTCTGCTGATGCA 755 : : : : : : : : :		03 03 03 03 03 03 03 03	2455 1176 2395 2395 2395 239027/c ABA19027 ABA19027; 23-JAN-2C
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                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; fimunosouppressive; antilnflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialidepetic; antilocer; antilocer; anticorvulsant; antifungal; antiparastitic; cardiant: immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
        Human nervous system related polynucleotide SEQ ID NO 11358.
                                                                                                                                               2000US-0179065.
2000US-0180628
2000US-018664.
2000US-0186350.
2000US-0189874.
2000US-0199076.
2000US-0199123.
2000US-0205515.
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2000US-0215135.
2000US-0216647.
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2000US-0217487.
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2-AUG-2000;
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2000US-0236367
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(ABB14678-ABB18001) useful for preventing, treating or ameliorating (ABB14678-ABB18001) useful for preventing, treating or ameliorating conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune contins, (c) cardovascular disorders such as myocardial ischaemias; (c) cardovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and eparasitic infections diseases such as viral, bacterial, fungal and marsatite infections.
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                                                                                                                                                                                                                                               Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oute: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (ABA11004-ABA21534) and proteins
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                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 11358; 1701pp + Sequence Listing; English
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Pred. No. 2.1;
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les 52; Conservative
                                                2000US-0251868.
2000US-0251869.
2000US-0251989.
                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                             08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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AAK75576/c
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20-OCT-2000;
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20-OCT-2000;
20-OCT-2000;
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22
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Barash SC, Ruben SM;

WPI; 2001-483426/52

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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
csupplement the patients own production of (I). Additionally, (I)
coplynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoletic-related diseases, especially
cancers and cancer metastases of haematopoletic-derived cells. AAK64703
copenses and cancer metastases of haematopoletic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 AACGCTGGGAAAAGGGCACCTGCCATTAACACTCTCCGCTCATTCCCAGGTGTTCTGTC 584
                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mammalian receptor proteins related to cytokine receptors, useful for regulating cell development and for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immunomodulator; DNAX cytokine receptor subunit 3.2; DCRS3.2;
therapy; immunological disorder; drug screening; cell development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNAX cytokine receptor subunit 3.2 reverse translational DNA.
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                                                                                                   Disclosure; SEQ ID NO 30388; 3071pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5666 BP; 1450 A; 1247 C; 1332 G; 1637 T; 0 other;
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Matches 52; Conservative
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                                                              metastasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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WO200003006-A1
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                                                   The present sequence is human DNAX cytokine receptor subunit 3.2

(DCRS3.2) reverse translational DNA. DCRS3 gene is located on chromosome leppla. Cytokine receptors, fragments and antibodies are useful for treating immunological disorders. DCRS3 (50R), DCRS4 (cytor) cor fragments are useful in drug screening to identify compounds having binding affinity to the receptor subunit. Modulators of DCRS are useful for modulating the physiology or development of a cell or tissue culture cells. A purified DCRS is useful as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to production of antibody to the endogenous receptor. Cytokine receptor sequences are useful as probes for detecting levels of the cytokine receptor in patients uspected of having an immunological disorder. Antibodies have therapeutic value, are useful as potent antagonist, in detecting or quantifying ligands, for isolating DCRS proteins and peptides, to screen expression libraries for particular expression products, to raise anti-idiotypic antibodies and for detecting or diagnoshiny various immunological conditions related to expression of the protein or cells which express the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1003 GTCCTGCTATATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCC 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .063 CGATAATCCGTCGAAGTCTGAGGATGGAAGGAAGGTGAAGGCTGTTCCTGAAAGGAATAA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883 GIGAGAIAGGCACAACAAIGAAAICACACAGAIAAIICAGGGAAAACGIICTGGICTIAC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAAYYTNCAYCCNWSNACNYTNACNYTNACNTGGCARGAYCARTAYGARGARYTNAA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPS-like enzyme; glucosyl donor substrate; sucrose; sucrose phosphate; tobaco; itce; carbon partitioning; growth response; CDP-qlucose-dependent sucrose-6'-phosphate synthesis; sucrose-6'-phosphate synthesis; sucrose-6'-phosphate; nucleoside diphosphate glucose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTGATGTAGGTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 RGAYGARGCNACNWSNTGYWSNYTNCAYMGNWSNGCNCAYAAYGCNACNCAYGCNACNTA
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "sucrose phosphate synthase-like enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                       3.0%; Score 35.6; DB 22; Length 1614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme;
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 30.3%; Pred. No. 1.2;
les 73; Conservative 34; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                           Sequence 1614 BP; 206 A; 189 C; 302 G; 202 T; 715 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a sucrose phosphate synthase-like enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sucrose biosynthesis; sucrose phosphate synthase-like
                             Disclosure; Page 18; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 1..2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ61263 standard; DNA; 2163 BP
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immunological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fructose-6-phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1123 A 1123
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The present sequence encodes a sucrose biosynthesis polypeptide which has a sucrose phosphate synthase-like (SPS-like) activity. The SPS-like polypeptide does not utilize UDP-glucose as a sole glucosyl donor substrate. Probes and amplification primers based on the SPS-like polynucleotide can be used to isolate or detect nucleic acid molecules which encode a protein with SPS-like activity. The SPS-like polynucleotide can be used to alter the level sucrose or sucrose phosphates in a plant cell, tissue, or organ or a higher plant, especially tobacco or rice. The SPS-like polynucleotide can also be used to alter the carbon partitioning, development and/or growth response of a plant, increase the level of UDP-, ADP- or CDP-glucose-dependent sucrose-6'-phosphate synthesis, and to produce sucrose-6'-phosphate from a nucleoside diphosphate glucose other than UDP-glucose in a plant cell. Recombinant SPS-like activity expressed in E. coll shows a broader specificity than the higher plant SPS increase as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1169 CCATTCTGACAATTTTGATAATATCCACCGGCCCCCATCCTCCGTGGCCACAATGGGC 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 ACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids encoding sucrose phosphate synthase-like enzymeuseful for altering the level of sucrose or sucrose phosphates and altering carbon partitioning in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.0%; Score 35.6; DB 21; Length 2163; Best Local Similarity 54.6%; Pred. No. 1.4; Matches 71; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein encoding DNA #40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2163 BP; 557 A; 517 C; 543 G; 546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucosyl donor to fructose-6-phosphate.
                                                                                                                                                                                                                                                    (CSIR ) COMMONWEALTH SCI IND & RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Page 91-95; 99pp; English.
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                                                                                     99WO-AU00557
                                                                                                                                                                  98AU-0004578
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                                                                                                                                                                                                                                                                                                                                     Furbank R, Lunn J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY69235
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                                                                                     08-JUL-1999;
                                                                                                                                                                  08-JUL-1998;
20-JAN-2000
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Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                 Bacillus licheniformis genomic sequence tag (GST) #1702.
                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVOZYMES BIOTECH INC. (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                   06-OCT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                   05-OCT-2001; 2001WO-US31437
 13-AUG-2002 (first entry)
                                                                                                                                Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                      Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                        4PI; 2002-416684/44.
                                                                                                                                                                   40200229113-A2.
                                                                                                                                                                                                    11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                      Berka R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acressimminogenic polypeptides. The proteins and their associated by a sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acres. The disorders include SAPHO syndrome (synovitis, acre, pustulosis, hypertosis and categories of medical conditions caused by P. acres. The disorders include SAPHO syndrome (synovitis, acre, pustulosis, hypertosis and categories of properties of the categories. P. acres is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acre vulgaris. A method for detecting the presence or absence of P. acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigonis and protein of antibodies specific for P. acres proteins. These antibodies can be used to downregulate expression and activity of P. acres polypeptides and determining P. acres infections. The antibodies spoil in ANU49156-AANU9883 and AANU5752-AANU5753.

Categories shown in AAU49156-AANU9883 and AANU5752-AANU5753.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed in the lactronic format directly from WIPO at the printed in the patient as a for the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 ATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACC 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                     polypeptides and nucleic acids useful for diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61313 BP; 10582 A; 18175 C; 19919 G; 12633 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAS59506-AAS59804 represent DNA molecules encoding
                                                                                                                                                                                                                                                   Mitcham JL, Wang SS, Bhatia A;
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 40; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53929 ACTCCGAAGACTCCGAATCC 53909
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                                                                                                                                              21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                               20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                   L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.4v
Tocal Similarity 53.4v
Tocal Similarity 53.4v
                                                                                                                                                                                                                                                                                                                                                                      treating acne vulgaris -
                                                                                                                                                                                                                                                   Persing DH,
                 Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                  WPI; 2001-616774/71
                                              WO200181581-A2.
                                                                                                                                                                                                                                                   Skeiky YAW,
                                                                                 01-NOV-2001
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in coher Bacillus cells. Comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells to expression of the same genes to one or more second Bacillus cells. The method is useful for monitoring genes in one or more second Bacillus cells. The method is useful for monitoring genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions.

The whole bacillus cells adapt to changes in culture conditions, convironmental stress or other physiological provocation. Extensive equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 CATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      967 CGTCTCCCTGCGGAACCAAAAATCCGTTCACGCCTCTTGAATGACTTCCCGGTGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 CCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGTTCAGCCAGTACCAA
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Pred. No. 1.5;
0; Mismatches 80; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 ACGUTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1135 BP; 322 A; 263 C; 298 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                       Claim 4; SEQ ID NO 1702; 200pp; English.
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50.9%;
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Best Local Similarity 50.9%
Them 83, Conservative
sequenced tag array
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ABK74411/c ID ABK74411 standard; DNA; 1135 BP.

RESULT 42

ABK74411;

AAK81290 standard; DNA; 21410 BP.

07-NOV-2001 (first entry)

AAK81290;

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AAK81290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oilgo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 TCCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAATATCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
      847 GCCCTTCCCTGATGCTTGAGGCGACAGACACGTCTGCAAGCTG 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 GGTACTCAATATCTTCTGGCGCTGGCTGCCATCATCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 CSRACIGGICATATCCTITIGAAGACIGCCTICAIRATAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 355 BP; 90 A; 67 C; 68 G; 119 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein 5' EST, SEQ ID NO: 26063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 26063; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; chromosome mapping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression and secretion vectors.
                                                                                                                                                                         AAC21988 standard; cDNA; 355 BP.
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                                                                                                                                                                                                                                                                                                     06-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                          AAC21988/c
                                                                                                           RESULT
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RESULT 44

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36102.
                                                                                                                                                                                                                                                                                                          2000US-0232397
                                                                       17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                14-AUG-2000; 2000US-022
                                                      WO200157182-A2
                                                                                                                                                                                                                                                                             08-SEP-2000;
                                              Homo sapiens
                                                                                                                                                                                                                               23-AUG-2000;
                                                                                                                                                               AUG-2000;
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                                                                                            02-MAR-2000
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14 - SEP - 2000; 21 - SEP - 2000; 21 - SEP - 2000; 22 - SEP - 2000; 22 - SEP - 2000; 22 - SEP - 2000; 22 - SEP - 2000; 23 - SEP - 2000; 24 - SEP - 2000; 25 - SEP - 2000; 26 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - S
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17 - NOV - 2000;
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17 - NOV - 2000;
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14-SEP-2000;
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17-NOV-2000
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AMANASIA TO AMANASIA. GARAGUE LIRE NUMBER NUMBER OF AMANASIA CANDERS AND AND AND AMANASIA. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) complement the patients own production of (1), Additionally, (1) complement the patients own production of (1), by inserting the call in a patient of protein and polynucleotides may be used to produce the secreted (1), by inserting concern and activity and polynucleotides may be used to prevent.

Concers and cancer metastases of haematopoletic-derived cells. AAK64703 cto AAK87694 represent inwention. AAK84942 to AAK8995 and AAM82169 represent invention. AAK84942 to AAK8995 and AAM82169 crepresent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9519 AGCTGAGATCATGCCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACTCCATCTCAAAA 9578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AGCTGAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 CAATGTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTCGGGCTGAAAAGAG 175
                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tyrosine phosphatase subfamily; cellular process modulation; phosphatase; chromosome 14; single nucleotide polymorphism; SNP; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 36102; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21410 BP; 6408 A; 3742 C; 4370 G; 6890 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.9%; Score 34.2; DB 22; Length Best Local Similarity 52.4%; Pred. No. 16; Matches 75; Conservative 0; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 GATCCGCCGTTATCTGTTGCATT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD15256 standard; DNA; 74962 BP
                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                            08-DEC-2000; 2000US-0251869
08-DEC-2000; 2000US-0251989
08-DEC-2000; 2000US-0251990
11-DEC-2000; 2000US-0254097
                                                                           2000US-0251868
                                                                                                                                                                                 2001US-0259678
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                                                                                                                                                                                                                                                               Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                   WPI; 2001-483426/52.
                                   06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                 05-JAN-2001;
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<pre>/standard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 16" replace (21652, T)</pre>	<pre>/*tag= t /standard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 17" replace (26291, T)</pre>	/*tag= u //standard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 18" /note= "Polymorphic site 28" /note= (28012, C)	/ctd=" /ctd="	/standard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 20" /eplace (33671, C)	/standard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 21" 3411134143 /*tag= y	3414435683 'teg= z 3568435737 /*teg= aa	3573839940 /*tag= ab replace (37703, G) /*tag= ac	e="Single nucleotide polymorphism orphic site 22" 3, G)	'standard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 23; This position is given as 39269 in the specification" /####################################	4003945810 /*tsg= af 45811.45871 /*tsg= ag	4587246578 /*tag- ah 46579.46615 /*tag- al	4 4	47043.4713 47134.47184	/"Lag= 47185.48943 /*tag= an 4894449016	/*tag= ao 490757568 /*tag= ap /756957602	57603.57761 /*tag= ar /*tag= ar /*tag= ar	
FT FT variation		FT FT variation	FT FT FT variation	FT FT variation	FT FT FT exon FT	FT intron FT Exon	FT intron FT variation FT	FT FT variation FT	FT FT FT exon	FT intron FT exon FT	FT intron FT exon	FT intron FT exon	FT intron FT exon	FT intron FT exon	FT intron FT exon	FT intron FT exon	F1 XX WO200160992-A2 XX XX 23-AUG-2001.
·	_		u.										(<u></u>		. (
	Location/Qualifiers 1936459833 /*tag= a /rochert = Human phosphatase protein"	replace (3114, A) /*tag= b /standard_name= "Single nucleotide polymorphism (SNP)" /note= "bolymorphic site 1"	replace (4004, A) /*tag= c /*tandard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 2"	replace (4514, G) /*tandard_name= "Single nucleotide polymorphism (SNP) /note= "Polymorphic site 3"	replace (7570, G) //tag= //tag= /standard_name= "Single nucleotide polymorphism (SNP)" //note= "Polymorphic site 4" replace (1572, G)	/*tag= [//*tag= [//*t	replace (1097, C) /*tag= g /standard_name= "Single nucleotide polymorphism.(SNP) /note= "Polymorphic site 6"	replace (#923, C) /*tag h // *tag h // *tag h // *tag h // *tag h // *tandard name= "Single nucleotide polymorphism (SNP) // */ */ */ */ */ */ */ */ */ */ */ */	/*tag 1 /*tag	<pre>/*tag= 1 /stag= 1 /stadard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 9" replace (17969, G)</pre>	<pre>/*cag= k /*tag= k /stadard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 10" replace (18117, T)</pre>	/"cay" / "cay" / // / // // // // // // // // // // /	<pre>/*tag= m //standard_name= "Single nucleotide polymorphism (SNP)" //note= "Polymorphic site 12" 1936419420</pre>	/*tag= n 19421.34110 /*tag= o	/*tage p // factor n/ /*tage p // /*tage p // /*tandard_name= "Single nucleotide polymorphism (SNP)" // // // // // // // // // // // // //	<pre>/*tag= q /stad=rame="Single nucleotide polymorphism (SNP)" /note="Polymorphic site 14" replace (20999, T)</pre>	/*tag-r r /single nucleotide polymorphism (SNP)" /standard_name= "Single nucleotide polymorphism (SNP)" /note= "Polymorphic site 15" replace (21465, G) /*tag= s
Homo sapiens.	Key CDS	varlation	variation	variation	variation		Variation	variation variation	variation	variation	variation	variation	exon	intron	variation	variation	variation
XX SO	HLL	FFFF	er Fr	FT FT FT	er Fr Fr				FFFF				FE	FT FT		FFF	

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Zea mays subsp. mays.
                          Drmanac RT, Liu C,
                                                 WPI; 2001-639362/73
  (HYSE-) HYSEQ INC.
                                                             P-PSDB; ABG06403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       their polynucleotides. The phosphatase proteins are related to the protein tyrosine phosphatase subfamily. The peptides of the invention are useful for identifying a modulator of phosphatase peptide expression. Modulators of phosphatase peptide are useful for treating diseases or conditions mediated by a human phosphatase protein. The phosphatase gene of the present invention can be expressed in yeast to identify possible interactors and substrates. Artificially synthesised enzymes or derived by this phosphatase. The present sequence is a human gene encoding phosphatase protein. This gene is located on human chromosome 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                        56 AGCTGAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 CAATGTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTCGGGCTGAAAAGAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                        New phosphatase peptide for the screening of modulators useful for
                                                                                                                                                                                                                 The present invention provides phosphatase peptides, proteins and their polynucleotides. The phosphatase proteins are related to the
                                                                                                                                                                                                                                                                                                                                                                 Sequence 74962 BP; 21639 A; 14055 C; 14307 G; 24824 T; 137 other;
                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 74962;
                                                                                                                                                                                                                                                                                                                                                                                                                68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #6394.
                                                                                             Di Francesco V, Beasley EM;
                                                                                                                                                                                                                                                                                                                                                                                      2.9%; Score 34.2; D
52.4%; Pred. No. 32;
1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5691 GAAACTCTGTCATTTGTGACAAT 5713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GATCCGCCGTTATCTGTTGCATT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS70590/c
ID AAS70590 standard; cDNA; 645 BP
                                                                                                                                                                                             Claim 4; Fig 3; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631,
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2000US-0649167.
           12-FEB-2001; 2001WO-US04432
                                   14-FEB-2000; 2000US-0182194
11-OCT-2000; 2000US-0685853
                                                                                                                                                                    treating related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.4
Matches 75; Conservative
                                                                                              Ketchum KA,
                                                                                                                     WPI; 2001-529910/58
                                                                       (PEKE ) PE CORP NY
                                                                                                                                  P-PSDB; AAE08552
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and conting sequences of the invention.

Continuous and acquences of the invention of mutations changed and products dependent on but and adaptostic coding sequences of the invention to several plant of the printed conting sequences of the invention of contactly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.9%; Score 34; DB 23; Length 645; 61.1%; Pred. No. 2.3; tive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 645 BP; 150 A; 182 C; 189 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 GCGCTGGCTGCCATCATCCGGAAGCGTTCC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 6394; 103pp; English.
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Tang YT;
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Best Local Similarity 61.19
Matches 55; Conservative
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US-0121825 US-0123180 US-0123348 US-0123788 US-0126786 US-0126786 US-0128714 US-0128714 US-0130370 US-013041 US-013051 US-013041 US-013051 US-013051	9905-0132484. 9905-0132485. 9905-0132486. 9905-0132863. 9905-0134256. 9905-0134218. 9905-0134218. 9905-0134218. 9905-013470. 9905-013470. 9905-013523. 9905-013523. 9905-013522. 9905-013629. 9905-013629. 9905-013629.	18-013949 18-013949 18-013945 18-013945 18-013945 18-013946 18-013946 18-013946 18-013946 18-013946 18-013946 18-013946 18-01396 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-01398 18-014288 18-014288 18-014288
-FEB-1999 -MAR-1999 -MAR-1999 -MAR-1999 -APR-1999 -APR-1999 -APR-1999 -APR-1999 -APR-1999 -APR-1999 -APR-1999	MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999 MAX-1999	2. JUNE 1. JUN
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PR 13-JUL-1999; 99US-01443624.
PR 14-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144006.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144322.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144332.
PR 22-JUL-1999; 99US-0144814.
PR 22-JUL-1999; 99US-0144614.
PR 22-JUL-1999; 99US-014508.
PR 23-JUL-1999; 99US-0145142.
PR 23-JUL-1999; 99US-0145142.
PR 23-JUL-1999; 99US-014519.
PR 27-JUL-1999; 99US-014519.
PR 27-JUL-1999; 99US-014519.
PR 27-JUL-1999; 99US-014519.
PR 03-AUG-1999; 99US-014519.
PR 03-AUG-1999; 99US-0144319.
PR 04-AUG-1999; 99US-0144319.
PR 13-AUG-1999; 99US-0144319.
PR 13-AUG-1999; 99US-0144319.
PR 13-AUG-1999; 99US-0144319.
PR 13-AUG-1999; 99US-0144319.
PR 27-AUG-1999; 99US-014491.
PR 27-AUG-1999; 99US-014491.
PR 27-AUG-1999; 99US-014491.
PR 27-AUG-1999; 99US-014491.
PR 27-AUG-1999; 99US-01499.
PR 27-AUG-199

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2000US-0225757.
2000US-0225758.
2000US-0225759.
                      17-JAN-2001; 2001WO-US01354
   09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 CCCGGTGGAATAACCGTTACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATG 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           762 GCGTGGATATGCAGGGGTAACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAA 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:5277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK60217 standard; cDNA; 333 BP.
990S-0157117.
990S-0157865.
990S-0158029.
990S-0158029.
990S-0158029.
990S-0159293.
990S-0159294.
990S-0159294.
990S-015930.
990S-015930.
990S-015930.
990S-0159637.
990S-0159637.
990S-0160767.
990S-0160767.
990S-0160767.
990S-0160780.
990S-0160980.
990S-0161406.
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AAK60217
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P-PSDB; AAM87436.

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(HUMA-) HUMAN GENOME SCI INC
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08-NOV-2000)
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08-NOV-2000)
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02-0CT-2000;
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02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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20-0CT-2000;
20-0CT-2000;
                                                       20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
cartivity, and can be used in gene therapy and vaccine production. (I)
cartivity, and can be used in gene therapy and vaccine production. (I)
proteins and polypuclectides may be used in the prevention, diagnosis and
cexample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynuclectides may be used to product the secreted (I), by inserting
colynuclectides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
concers and cancer metastases of haematopoletic-related diseases, especially
cancers and cancer metastases of haematopoletic antigen genomic
concers from the present human immune/mematopoletic antigen genomic
sequences from the present humaniammune/mamatopoletic antigen genomic
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 GGAAAACCGCTGAACAAAATTCGGGCTGAAAAGAGGATCCGCCGTTATCTGTTGCATTTC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 CCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCCGTTCTGTTAATATCAAACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 GGAAAGAGATAGAGGGAAGGTGGTGTTGCAATCAGACTGGACAGCTTCATGTCCCTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.8; DB 22; Length 333;
Pred. No. 1.9;
2; Mismatches 64; Indels 0;
                                                                                                    Claim 1; SEQ ID NO 5277; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 333 BP; 71 A; 88 C; 77 G; 93 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 48858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV48867 standard; cDNA; 474 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 CCCTCTTCATCTCATCT 235
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2000US-211314P.
2000US-219007P.
2000US-255281P.
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Best Local Similarity 51.8%;
Matches 71; Conservative
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16-MAR-2000; 2000US-189862P.
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18-JUL-2000;
13-DEC-2000;
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                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GAGATGGAAAAAAAGCCAAAATAAAAATTGCCCATCCCAGCGCGCTCCAGCTGAAAGTA 66
                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -

    (c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
    (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 GCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTTGTTTACAACGTCGTGA 354
                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                               (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                 2.9%; Score 33.8; DB 23; Length 474;
55.6%; Pred. No. 2.3;
1ve 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fourette Syndrome; TDO2; kyneurenine formation; autism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Tryptophan-2,3-dioxygenase coding sequence HTO3.
                                                                                                                                                                                                                                                                                                                                                         Sequence 474 BP; 140 A; 114 C; 118 G; 102 T; 0 other;
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                         Claim 1; Page 9566-9567; 11750pp; English
                       Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ21621/c
ID AAQ21621 standard; DNA; 1647 BP
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34..1008
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                           65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                 WPI; 2001-662795/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-1991;
                      Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-1991;
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                                                                                                                                                                                                                                                                                                                     patient;
                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The specification includes two different sequences which are the specification includes two different sequences which are the specification includes the stage AAQ21620). They are identical through the first 741 nucleotides of AAQ21620 before the much longer sequence AAQ21621 begins to diverge. The human TDO2 gene sequence, including regulatory sequences, is also given in the specification, as is a genomic TDO2 sequence which includes the introns (see AAQ2162) and AAQ21624, respectively). The sequence of the open reading frame in these sequences defices from AAQ21620) by the deletion of a single adenine residue (i.e. from the run of 8 A's at position 713-720 of AAQ21621). Yet another Figure, which illustrates the asingle of homology between HTO3 and the rat TDO2 sequence, also lacks the 8th Adenine, suggesting that the "extra" A in both AAQ21620 and AAQ21621 represents a typographical error. The patent specification does not contain any discussion of the apparent differences and includes only the minimum description of each of the sequences. Consequently, the significance of an in frame contains the longest CDS of HTO3 is not known.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1013 ATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCG 1072
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                                                                                                                                Diagnosis of Tourette syndrome and associated disorders - by detecting mutation in tryptophan oxygenase-indole:amine oxygenase
                                                                                                                                                                                                                                                                                                                                                                                         Clone HTO3 was isolated from a human liver mRNA-derived cDNA library screened with a rat liver tryptophan oxygenase cDNA probe
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Best Local Similarity 53.4%; Pred. No. 4.7;
Matches 71; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                               Disclosure; Fig 5A; 45pp; English.
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WPI; 1992-080090/10.
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                                                  P-PSDB; AAR21547
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15.1.6 5.1.6 1.0
Copyright (c) 1993 - 2003 Compagen Ltd. OM nucleic - nucleic search, using sw model Run on: June 18, 2003, 01:20:59; Search time 1249.12 Fittle: US-09-674-277-2 Scoring table: US-09-674-277-2 Sequence: 1181 Sequence: 16154066 seqs, 8097743376 residues Fortal number of hits satisfying chosen parameters: 32308 Minimum DB seq length: 0 Maximum Match 100% Maximum Match 100% Maximum Match 100% Maximum Match 100% Maximum Match 100% Maximum Match 100% Maximum Match 100% Maximum Match 100% Maximum Match 100% Maximum Match 100% Listing fifst 150 summaries EST:* Sem_estba:* Sem_estba

RESULT 1 A0989708 LOCUS LOCUS DEFINITION RfC00285 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens strain W14 M13 library ACCESSION A0989708 REYWORDS REYWORDS SOURCE ORGANISM Photorhabdus luminescens ORGANISM Photorhabdus luminescens ORGANISM Photorhabdus luminescens Photorhabdus luminescens ORGANISM Photorhabdus luminescens Photorhabdus luminescens Photorhabdus luminescens ORGANISM Photorhabdus luminescens Photorhabdus luminescens Photorhabdus luminescens ORGANISM Photorhabdus luminescens	REFERENCE 1 (Dases 1 to 755) AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. TITLE A genomic sample sequence of the entomopathogenic bacterium photorhabdus luminescens W14: potential implications for virulence JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000) MEDLINE 20378633 COMMENT Department of Blology and Blochemistry University of Bath South Bullding, Bath BAZ 7AV, UK Tel: (44) 1225 826739 Email: bssrfc@ath.ac.uk This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. colls K12 genome) please see ffrench-Constant et al. 2000, Nucleic Seq primer: M13 Forward	fiers torhabdus luminescens" 1.29488" 65" otorhabdus luminescens stri imary phase variant" DNA from strain W14 was s: loned into M13 Janus." 36 g 209 t 12 foneth	Docal Similarity 54.5%; Pred. No. 0.011; ss 120; Conservative 0; Mismatches 264 TCAATATCTTCTGGGGGTGGCTGCCATCATCGG 53 TCAATCGTTGACGGCTGGTTTTCCCATTTTTGG 324 TCGCCAGTGCAGCGGTTTTCCCATTTTTGG 325 TCGCCAGTGCAGCGGTTTTCCCATTTTTGG 326 TGGCCAGTGCAGCAGTGCAGAACTCCGGTAATGTTTTGGAATGACAGTTCCGGTTGAATGCGCCGGTGGAATGCTCGGAATGCTCGGTAAGGTTGGAATGCTCCGATAGGAATGCTCAAACGTI
BF341523 602013526 AZ377715 1M0126A03 BG565053 602583848 BF0020591 8m51a12. Y B1833613 603088306 AV647553 AV647553 AV655093 AV655093 BG562641 602581421 AV65534 AV655934 BG5628115 602572494 BG565118 602583444 BG565318 602583484 BG565314 602583535 BG565877 602583532 BG565877 602583532		BG533516 601860931 BE380004 601159314 BG370004 601159314 AL437003 To end of AL108631 Drosophil AL43703 Tr end of AQ110329 CIT-HSC-2 AU056834 AD056834 BF860318 963016C03 AL064634 Drosophil AL055400 Drosophil BG026002 602292170 AA196883 zg60607.r A1858306 w136a11.x B1961758 W0W01_4.C	BG50596 60185935 BF241131 601859324 BG491140 602540545 BG491140 602540545 BG492140 602540545 BG49236 GSSBTU088 BM30341 IDU033B.1. BM871377 bm71b05.9 AW658701 95329 MAR BM35662 A Ea002 BG443931 GA Ea002 BG443931 GA Ea002 BH36032 CH230-107 AQ746896 E01864437 AL186955 Tetraodon BG106295 60289649 AL270439 Tetraodon BG106295 602289649 AL270439 Tetraodon AL073830 Drosophil BG892595 fq75907.x AW530608 U.RC4-a BJ458049 BJ458049
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8 8 8 8 8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9	. <i>.</i>	1114 11116 11117 11122 1122 1122 1224 1224 1224 12	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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/organism="Hordeum vulgare subsp. vulgare"
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                                                                                                     Hordeum vulgare subsp. vulgare.

Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Hordeum.

1 (bases 1 to 615)

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases I to 629)
0ghbra, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
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Pred. No. 0.043;
0; Mismatches 69; Indels 0
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                                                                                                                                                                                                                                                                                                                     1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akashinriki vegetative stage leaves /tissue_type="leaves"
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National Institute of Genetics
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118 c 193 g 141 t
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Location/Qualifiers
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BJ264853.1 GI:20085028
                                                                       AV909088.1 GI:18204518
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Best Local Similarity 56.1%;
Matches 88; Conservative (
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/urian "Triticum aestivum"
/cultivar="Chinese Spring"
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/dultivar="Chinese Spring"
/clone="whi9524"
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/tissue_type="spike at heading date"
/dev stage="spike at to Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from the two samples, polyA was purified from the pooled from the two samples, polyA was purified from the pooled from the two samples, polyA was purified from the pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin Choi, Close, Fenton, Rianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
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1 (bases I to 669)

2sto, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Email: tshini@genes.nig.ac.ip.
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56.1%; Pred. No. 0.043;
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Location/Qualifiers
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                           BJ312175 Y. Ogihara unpublished cDNA library, Wh_yd Triticum aestiyum cDNA clone whyd24j0l 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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431 GGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGG
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1 (bases 1 to 647)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Coetion.Coulifiers
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                 BJ312175
BJ312175.1 GI:20119140
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Hordeum vulgare subsp. spontaneum.

Hordeum vulgare subsp. spontaneum

Hordeum vulgare subsp. spontaneum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;

Triticeae; Hordeum.

1 (bases I to 693)

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV945422 K. Sato unpublished cDNA library, strain H602 adult, adv945422 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah26115 3', mRNA sequence.

AV945422 GI:18241219
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/tissue_type="top three leaves"
/tissue_type="adult, heading stage"
1 204 c 175 t 1 others
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    693
/organism="Hordeum vulgare subsp. spontaneum"

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Pred. No. 0.044;
0; Mismatches 69; Indels
                                                                                                                                                                                                                                                            Indels
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fex: 81-559-81-6856
                        /db_xref="taxxxx:112509"
/clone="baak11122"
/clone=lb==k. Sato unpublished cDNA
Akashinriki vegetative stage leaves"
/tissue_type="leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 CATGACCACCACACTGGCAATCCGGTAGACCGGTAAC 527
                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                    DB 10;
                                                                                                                                   /dev_stage="vegetative stage"
202 c 135 g 171 t
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Pred. No. 0.043;
0; Mismatches (
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/db_xref="taxon:77009"
          cultivar-"Akashinriki"
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Location/Qualifiers
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Best Local Similarity 56.1%;
Matches 88; Conservative
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56.1%;
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nes 88; Conservative
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Oryza sativa (japonica cultivar-group).

Sukaryota: Viridalplantae: Streptophyta: Embryophyta; Tracheophyta: Bukaryota: Viridalplantae: Streptophyta: Embryophyta; Tracheophyta: Spermatophyta: Magnoliophyta: Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Ehrhartoideae; Oryzeae; Oryza.

Sasaki, T. and Yamamoto.K.

Rice cDNA from callus (2000)

Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
705-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH468052 866 bp DNA linear GSS 13-DEC-2001
BOHOJ24TF BOHO Brassica oleracea genomic clone BOHOJ24, DNA
sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 866)
Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
(Dnpublished (2001)
Other_GSSs: BOHOUZ4TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 ACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 GCCATGGACTCCAGCACTACTTGACCAAGTGTCTCAGATCTGAAGGCATTGCAAACAAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="C12279"
/clone_lib="Rice callus"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid. "
147 c 186 g 178 t
                                                                                                                                                                                                                                                                                                                                                                              Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 ITCTICIGAAIGACAICAGGGAICCCGCCCGICICACIGGCGAIAACGGGCACGCCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%; Score 42.2; DB 9; Length 714; 55.9%; Pred. No. 0.77; tive 0; Mismatches 63; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
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Best Local Similarity 55.99
Matches 80; Conservative
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1 (bases 1 to 495)

1 (bases 1 to 495)

1 Hedley, P. Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.

1 Dupublished (2001)

1 Contact: Waugh R. Marshall DF Genome Dynamics/Computational Biology

2 Scottish Crop Research Institute

Invergowite, Dundee, DD2 5DA, Scotland, UK

Tel: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: psporn; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pspoRT1.
Derived from roots of 3 week old waterlogged barley plants. Developed as part of the barley transcriptome resources of BBSRC/SERRAD funded cereal IGF (Investigating Gene Function) project.

1 176
                                                                                  EBro03_SQ005_K13_R root, 3 week, waterlogged, cv Optic, EBro03 Hordeum vulgare cDNA clone EBro03_SQ005_K13 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taptor:4513"
/db_xref="taptor:4513"
/clone="EBro03_SQ005_K13"
/clone_lbp="root, 3 week, waterlogged, cv Optic, EBro03"
/tissue_lype="root"
/dev_stage="a week"
/lab_host="DH10B"
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714 bp mRNA linear EST 03-APR-20
MU100720 Rice callus Oryza sativa (japonica cultivar-group) cDNA
clone C12279, mRNA sequence.
AU100720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"/cultivar="Optic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@scrl.sar1.ac.uk.
Location/Qualifiers
                                                                                                                                                                            BQ763870.1 GI:21972342
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                                                                                                                                                                                                                   Hordeum vulgare.
Hordeum vulgare
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                                         RESULT 7
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Gaps

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42; Conservative 118; Mismatches
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- Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

- Listation of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEBH (Centre d'Interdy (Dros BAC) was made by Alain With funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                          391 GAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 CTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAA 510
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 1101)
Genoscope.
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                                                                                                                                                                                                                                                                                                    Score 41.6; DB 17; Length 866; Pred. No. 1.2;
   Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
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/db_xref="taxon:7227"
/clone="BACN03K20"
                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                 /organism="Brassica oleracea"/strain="TO1000DH3"
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AL098595.1 GI:5610206
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/plasmid="pBeloBAC11"
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/clone_l1b="BOHO"
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Drosophila melanogaster
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Score 41; DB 17; Length 1101;

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Query Match

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ECORI; Site_2: XhOI; 3-4 days old root tissue from Walbot
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          941 ACGGGTGATGTAGGTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCT
                                                                                    881 GGGTGAGATAGGCACAACAATGAAATCACAGATAATTCAGGGAAAAACGTTCTGGTCTT
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/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/tlssue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
         Gaps
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Maize ESTs from various cDNA libraries sequenced at Stanford
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2227
Fax: 650 725 8221
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Pred. No. 2.1;
0; Mismatches
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Plate: 614026 row: D column: 01.
Location/Qualifiers
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/cultivar="W23"
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Best Local Similarity 55.2%;
Matches 79; Conservative (
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Seq primer: SP6
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Matches 82; Conserv
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 ITCTTCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 ACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACA 503
             438 TCCTTGGGTATTATCAGGTATCCCTCCAGCACGAGCAGCGACGACTGGGACTCCAGAA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 GCCATGGACTCCAGCACTACTTGCCCGAGGGTCTCGGATTCTGAAGGCATTGCAAATACA 557
ACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             functa-"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont configs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
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BQ087067
BQ087067.1 GI:20046268
                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 736)
Hainey.C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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Pred. No. 2.2;
0; Mismatches 64; Indels 0
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                                                                                                                                                                            mRNA
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/db_xref="MaizeDB:633031"
/db_xref="taxon:4577"
                                                                                                                                                                        AY112421 736 bp
Zea mays CL8980_1 mRNA sequence.
AY112421
                                                                                  181 TCCGCACTGCCGTACGCTTGTGA 159
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                                                            504 CTGGCAATCCGGTAGACCGGTAA 526
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198 c 154
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Best Local Similarity 55.2%;
Matches 79; Conservative
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Unpublished (2002)
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/organism="Ceratopteris richardii"
/organism="Ceratopteris richardii"
/db_xref="Laxon:4495"
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/cell_type="Gametophyte"
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/dev_stage="Sor
Ceratopteris richardii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Filicopsida; Filicopsida; Filicales; Pteridaceae; Ceratopteris.

Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.

E theses 1 to 645)

Expressed sequence tags of cont.S.C., Banks, J. and Roux, S.J.

Expressed sequence tags of cDNA clones from a C. richardii library Unpublished (2000)

Contact: Roux SJ

Section of Molecular Cell and Developmental Biology

Biology Building, Room 16, Austin, TX 78712, USA

Tel: 512 471 4238

Fax: 512 232 3402

Email: sroux@uts.cc.utexas.edu

Plate: Cri_9 row: I column: 06
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1 (bases 1 to 461)
Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D. Generfresher methylation filtered genomic sequences from maize Contact: Bedell JA.
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4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
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ilarity 53.6%; Pred. No. 4.7;
Conservative 0; Mismatches 71;
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Tissue Procurement: ATCC
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Best Local Similarity 52.1%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                           /organism="Zea mays"
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/rocyan: pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor pactor p
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.2; DB 17; Length 461; Pred. No. 5.1; 0; Mismatches 73; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGACCACACACTGGCAATCCGGTAGACCGGTAA 526
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                                        Email: jbedell@criongenomics.com
Plate: fzmb013f051 row: a column: 07
Seq primer: M13 forward
Class: shotgun
High quality sequence stop: 461.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Other_GSSs: AG-ND-130K10.TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH388561.1 GI:17334702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.3
Best Local Similarity 53.2
Matches 83; Conservative
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KEYWORDS
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TITLE
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ORIGIN
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BH388561
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926 bp mRNA linear EST 27-FEB-2001 602428912F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4558514 5', BG330039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Butheria; Hordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 926)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="retinoblastoma",
/lab_host="DH10B (phage-resistant)",
/lab_host="DH10B (phage-resistant)",
/note="Gorgan: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript IRT (Life Technologies).
Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1264 row: h column: 03
High quality sequence stop: 667.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      345 GCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGG
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                Length 769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 AGACCGAAGCTTTCCTGTTGTGACGGAAGCATAAATACATCCGCA 301
                                                                                  /strain="PES:
/db_xref="taxon:7165"
/clone="AG-ND-130K10"
/clone=lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                      79;
                            1. 769
/organism="Anopheles gambiae"
/strain="PEST"
                                                                                                                                                                                                                                                                                                Score 38.6; DB; Pred. No. 8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4558514"
/clone_lib="NIH_MGC_16"
Location/Qualifiers
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Gaps

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Indels

d. No. 11; Mismatches

Pred.

52.5%;

Conservative

383

324 TCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACA 373 TCAACCATTGCCTCGGCCAGCTTTATTCCATCGGTATCAGAAATCTTCGTCCCTGTCACT 384 ITCTICTGAATGACATCAGGGATCCCGCCGTCTCACTGGCGATAACGGGCACGCCGGAG

443

313 CCTTCAATAACTGTCTCTGAGGGCCCACCACTGTCAATAACAATAACTGGACGACGTTGC 254

ACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATT 481

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Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bohlapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 395.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI744669

509 bp mRNA linear EST 25-SEP-2001 rK89blO9.y1 Meloidogyne javanica egg pAMP1 v6 Chlapelli McCarter Meloidogyne javanica cDNA 5' similar to TR:022698 022698 SIMILAR TO GLYCOSYLITRANSFERASE ALG2. [1]; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotzi, Mctazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

1 (bases 1 to 509)
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y. Glbbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Renko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, M., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                               ö
                                                                                                                           702 TCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAACATTGTCTGCTGATGCAGCCCAG 761
                                                                                                                                                                                                                                821
                                                                                                                                                                                                                                                                             757 CTTAGGATCTTAAGAGGAAACAGTCGGATTTCTTCAACCGGAGCAGCAGGACGCCAGGAG 698
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/organism="Meloidogyne javanica"
/db_xref="taxon:6303"
/clone_lib="Meloidogyne javanica egg pAMP1 v6 Chiapelli
                                                                                                                                                                           817 TTGGGAAGCCCCCCCCCCCCCTCCAGGTCACCGGGCGCACTGAGTCCCGTGTTCACCAAT
                                                                                                                                                                                                                             762 GCGTGGATATGCAGGGGTAACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAA
                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Context: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington Univ. Nematode Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1810
                                                                               ö
                             Length 926;
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                                                                            Indels
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                                                                         83;
                             DB 12;
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/lab_host="DH10B"
                       Score 38.2; DE
Pred. No. 11;
0; Mismatches
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                       Query Match 3.2%;
Best Local Similarity 51.5%;
Matches 88; Conservative
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Meloidogyne javanic
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BI744669/c
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KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.; Triticeae; Triticum.

1 (bases 1 to 632)

2 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han Saton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library

L Upublished (2000)

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595818
                                                      BG605346 632 bp mRNA linear EST 16-APR-2001
WHE2331_F11_L202S Wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WHE2331_F11_L20, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site_1: EcoRI: Site_2: XhoI; Plants were grown in the Site_1: EcoRI: Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript the cDNA and colored in the TI close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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/db_xref="taxon:4565"
/db_xref="taxon:4565"
/clone="WHE2331_F11_L20"
/clone="Ib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers
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    632
    /organism-"Triticum aestivum"

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                                                                                                                                                                                                                      bread wheat.
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Matches 74; Conserv
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RESULT 18
                                                                                                                                      ACCESSION
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DB 13; Length 509;

Score 38;

3.28;

Query Match

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491 CATGACCACACACTGGCAATCCGGTAGACCGG
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performed in the OD Anderson and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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1 (bases I to 479)

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11 (bases In Triticum aestivum Unpublished (2002)

12 (contact: Tadasus Shin-1

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                            444 ACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACA 503
TICITCIGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAG 443
                                                                                                                                       130 GCCAIGGACTCCAGCACTACTIGTCCGAGGGTCTCAGACTCTGAAGGCAITGCAAATACG 71
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Fax: 81-559-81-6856
Email: tshini8genes nig.ac.jp.
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52.9%; Pred. No. 13;
:ive 0; Mismatches
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                                                                                                                                     /clone_lib="Rice panicle at ripening stage"
/dev_stage="ripening stage"
/note="Organ: panicle; Rice cDNA from panicle at ripening
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 545)
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Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E12053"
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84 CATIGCAAAIACGICCCCACIGGCAIACGCCIG 52
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Submitted (12-ARP-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.ons.fr/Tetraodon.

1. 756
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 649)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Teraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 756)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Benote, J., Fisher, C., Mincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 CATTALIGAAGIGGCIGIIGCAGCICIIGIAGIICAAICAAICIIIATIACCCIGGIGGG 274
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Roest-Crollius, H., Jalllon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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/note="Genoscope sequence ID : COAG256CH05SP1-end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="256P09"
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AV784670
AV784670.1 GI:19803460
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Matches 101; Conservative
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Large scale analysis of Arabidopsis full-length CDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-439
Fax: 81-298-
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MEST8-G12.T3 ISUM3-TL 2ea mays cDNA clone MEST8-G12 3', mRNA
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Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
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1 (bases 1 to 501)

Gluff., Cul.F., Guo.L., Ashlock, D.A, Wen.T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/db_xref="taxon.3702"
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/clone_lbb="RAFL66"
/dev_stage="plants at various developmental stages from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5, 10,
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Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
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/lab_host="DHIOB"
/note="Site_1: Sat1; Site_2: XhoI; subjected theydration (1, 2, 5, 10, 24 hr) and cold (1, hr) treatments"
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0; Mismatches
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52.6%;
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Best Local Similarity 52.6
Matches 81; Conservative
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BG840188.2
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Gaps

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FEATURES

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/organism="Sorghum propinguum"
/db_xref="taxon:132711"
/clone_lib="floral-induced Meristem 1 (FM1)"
/clone_lib="floral-induced meristems; Vector:
/clone_lib="floral-induced meristems; Vector:
/clone_lib="floral-induced meristems; Vector:
/clone_lib="floral-induced meristems; Vector:
/clone_lib="floral-induced meristems; Vector:
/clone induced in floral induced in floral induced in light (flowering is induced by short-day conditions): 16 days after being returned to the greenhouse under natural long days during late April/carly May, meristems were harvested The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
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Vodkin, L., Reim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)

Unpublished (1999)

Contex_ESTS: AW20345 corresponding to Gm-c1028-1235 (5')

Context: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI968888 672 Dp mRNA linear EST 23-OCT-2001 GM830006B20A01 Gm-r1083 Glycine max cDNA clone Gm-r1083-1946 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max
Mukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 GGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGG 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Illinois
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Fax: (217) 334-4582
Email: 1-vodkin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CTTACCCTCCTTGTCCTTGGGTATTATATCAGGTATCCCTCCAGCACGACGACAAC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Indels
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                                                                                                                                                                                                                                                                                                                                                 138 t
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/organism="Glycine max"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      mass excision.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.1%;
Best Local Similarity 56.1%;
Matches 69; Conservative
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BI968888
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BI968888
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum propinguum
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 540)
Cordonnier-Pratt, M. -M., Gingle, A., Sudman, M., Marsala, C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 ITCTICIGAAIGACAICAGGGAICCCGCCCGICICACIGGCGAIAACGGGCACGCCGGAG 443
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Far: 706 542 1860
Fax: 706 583 0210
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FMI_31_H07.g1_A003 Floral-Induced Meristem 1 (FMI) Sorghum
propinguum cDNA, mRNA sequence.
BF586903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An EST database from Sorghum: floral-induced meristems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.8; DB 12; Length 501; Pred. No. 25; 0; Mismatches 52; Indels 0
                               PCR PRIMERS
FORMARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 9
High quality sequence stop: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Cordonnier-Pratt MM
            Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF586903.1 GI:11679227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%;
56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                      source
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VERSION
KEYWORDS
SOURCE
ORGANISM
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RESULT 24 BF586903/c

셤 ò DEFINITION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

BASE COUNT ORIGIN

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511 TCCGGTAGACCGGTAAC 527
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ORIGIN
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Matches
TITLE
JOURNAL
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       /clone_lib="Gm-ri083.1946"
//clone_lib="Gm-ri084"
//clone_lib="Gm-ri094"
//clone_lib="Gm-ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI498039 499 bp mRNA linear EST 29-NOV-2001 sag15c08.yl Gm-c1080 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1080-1263 5' similar to TR:Q9R6U1 Q9R6U1 SQDX. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olympian (Dases 1 to 499)
Shoemaker,R., Kelm.P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marran,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Beck,C., Toderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 GAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 CTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 GGATTATATCAGGAATACCTCCAGCACNNNCCGGCACCACAGGTATCCCTGAAGACATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.4; DB
Pred. No. 33;
0; Mismatches
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Best Local Similarity 53.3%;
Matches 73; Conservative
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BI498039/C
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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/nab_nost=rububer
/nab_nost=rububer
/nab_nost=rububer
/note=vVector: pBluescript II SK+; Site_I: ECORI; Site_2:
Xho1; The mRNA was isolated from roots of 8 day old
'Bragg' supernodulating mutant NTS382 seedlings that were
infected with Bradylizobium japonicum, strain USDA 110, 72
hours prior to harvest. Dr. Gary Stacey generously donated
the tissue. The roots were flash-frozen in liquid
nitrogen. Stratagene's conka Synthesis Kit (catalog number
200401) was used to synthesize the cDNA. First-strand
synthesis was performed with 5-methyl dCTP, hence the
ligated CDNA was hemimethylated. A modification of
Stratagene's first-strand synthesis primer was used. An
anchor nucleotide (V-A, C, or G) was added to the 3' end
of the primer [GAGAGAGAGAGAGACACATAGTCTCGAG(T)18V] to
anchor the primer at the 5' end of the poly(A) tract.
After second strand synthesis, the CDNA ends were filled
in with cloned Pfu DNA, ligated to ECORI adapters and
subsequently phosphorylated. The CDNA was then
precipitated and redissolved in sterile, Rhase.,
DNAse-free water. The XhoI site within the first-strand
synthesis primer was then restricted by digestion with
XhoI from Promega (40Vul); all XhoI sites in the CDNA
would be protected by their hemimethylated status. The
CDNA constructs were size-fractionated with a 500bp
cutoff, using Sephacryl s-500 High Resolution (Pharmacia
Biotech) in a 2-mm diameter column and a bed volume of
approximately lml. The column eluent was precipitated,
redissolved, and ligated into Stratagene's pBluescript II
XR Predigested vector (obluescript II SK(+) vector that
has been digested with EcoRI and XhoI, and phosphorylated
laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at
Northern Arizona University."
                                                                                                                                                                                                                                                                                              This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 GAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACG
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Fublic Solved 1899)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Glycine max"
/db_xref="taxon:3847"
/db_xref="taxon:887"
/clone_ib="GENOME SYSTEMS CLONE ID: Gm-c1080-1263"
/clone_ib="Gm-c1080"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36.2; DE
Pred. No. 36;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 327.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="8 days old"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.1%;
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450

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Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 09-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare seedling leaves second leaf stage" /tissuc_type="seedling leaves" dev stage="second leaf stage" 7 others
                                                                                                                                                                                                                                                                                                            205 GGATTATATCAGGAATACCTCCAGCACGTGCCGCCACCACAGGTATCCCTGAAGACATCG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV836868 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare seedling leaves second leaf stage Hordeum vulgare subsp. vulgare cDNA clone basdll6, mRNA sequence.
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                                                                                                                                                                                                            391 GAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACG
                                                                                                                                                              Gaps
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Contact: Razuhiro Sato
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Contact: Razuhiro Sato
Contact: Razuhiro Sato
Contact: Razuhiro Sato
Contact: Razuhiro Bariey Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: Razsato@tib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/Darley,
database:http://www.shigen.nig.ac.jp/Darley/Barley.html.
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                                                                                                          Length 516;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare subsp. vulgare"
coultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="basd116"
                                                                                                                                                              Indels
                                                                                                                                                           63;
                                                                                                          DB 13;
                              122 t
                                                                                                                                                              0; Mismatches
                                                                                                          Score 36.2; Pred. No. 37;
University of Illinois)."
106 c 131 q 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV836868.1 GI:14528957
                                                                                                                                                                                                                                                                                                                                                                                                                           511 TCCGGTAGACCGGTAAC 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 TGGCATATGCTTGGGAC 69
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                                                                                                          3.18;
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Best Local Similarity 54.5
Matches 72; Conservative
                                                                                                             Query Match 3.1
Best Local Similarity 54.0
Matches 74; Conservative
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                                   157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
AV836868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: estéwatson.wustl.edu
his clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccuéresgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker, R. Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, Shoemaker, R., Kelm, P., Vodkin, L., Kucaba, T., Martin, J., Beck, C., An. Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Unpublic Soybean EST Project
                                                                                                                                     BM143281 516 bp mRNA linear EST 29-NOV-2001 saj42b12.y1 Gm-c1072 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1072-2375 5' similar to TR:Q9R6U1 Q9R6U1 SQDX. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="seedlings induced for symptoms of SDS (Sudden Death Syndrome) disease" /dev_stage="2-3 weeks old" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Www.resyen.com

Seq primer: -dORP from Gibco

High quality sequence stop: 421.

Location/Qualifiers

1. 516

/organism="Glycine max"
//db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1072-2375"
/clone_lib="Gm-c1072"
                                                                                                                                                                                                                                                     BM143281
BM143281.1 GI:17153348
                   TGGCATATGCTTGGGAC 232
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                                                                                                                                                                                                                                                                                                                                                             Glycine max
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452 490

512

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GSS 26-JUL-1999
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Not1: Site_2: Sal1; CDNA made by oligo-dT priming.
Locationally cloned using the following adaptors:
5'-TCGACCAGGCTCG-3' and
5'-TCGACCAGGCTCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1,7 kb. This. is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                   L Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13560 row: e column: 04
High quality sequence start: 62
High quality sequence start: 62
High quality sequence stop: 560.
I. 974
Corpanism="Homo sapiens"
// All xref="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence T7 end of BAC absolitol of DrosbAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 974)
NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="Lupski_dorsal_root_ganglion"
/kas="mage"="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH108"
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55.8%; Pred. No. 51;
ve 0; Mismatches
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BQ878757.1 GI:22270765
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Matches 52; Conservative
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GSS; genome survey sequence.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Materia Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Actinopterygii; Neoterygii; Percomorpha; Tetracdontiformes; Tetracdontidae; Tetracdon.

Tetracdontidae; Tetracdon.

E 1 (bases 1 to 849)

S Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Saurin, W. and Weissenbach, J.

Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using translation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscyer, Direct Submission
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clonne-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                         CNSU3IJD 849 bp DNA linear GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 029012 of library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Welssenbach, J.
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="029C12"
/clone=lib="G"
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Gaps

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350

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// Organism="Homo sapiens"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
//dclone="InhAGE:472378"
//clone=lib="NHH MGC_76"
//lab_host="DHIOB (TI phage-resistant)"
//ncte="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
//ncte="Organ: liver; Vector: pDNR-LIB (Glontech); Site_1:
//ncte="Organ: liver; Vector: pDNR-LIB (Glontech); Site_1:
//ncte="Organ: liver; Vector: pdn as follows: 5" adaptor
3' adaptors were used in cloning as follows: 5" adaptor
3' adaptors were used in cloning as follows: 5" adaptor
5' -ATTCTAGAGGCCGCAGAGGCATG-0T(30) NN-3' (Where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG565743 110-APR-2001
602589078F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4723338 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 ACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTGTGAATGACATCAGGGATCCCG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 ACATCAACTACCTGGACAGAACACCCCCAACCGCCGCTGCGCACCATCAAGGGTCACA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dasas 1 to 831)

NIH-WGC http://mgc.ncl.nih.gov/.

NIH-WGC http://mgc.ncl.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                /db_xref="taxon:7955"
/db_xref="taxon:7955"
/clone_lib="zebrafish Embryonic Heart cDNA Library"
/dev_astage="embryonic day 3 post-fertilization"
/dev_astage="coli Xil-Blue mrF'"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_l:
FcoRi; Site_2: Xhoi; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). CDNA was
synthesized using a Xhoi-Oligo dT adaptor-primer. EcoRi
adaptors were ligated, followed by digestion with Xhoi,
for directional cloning into pre-digested lambda ZAP
Fwress vertor. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lihl.gov.k.column: 19
Plate: LLCM1582 row: k.column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 ATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAGTGCGCCGGTCCATGCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 CCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTAC 463
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Location/Qualifiers
              /organism="Danio rerio"
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94 c 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW453731 320 bp mRNA linear EST 17-FEB-2000 zehl0506 Zebrafish Embryonic Heart cDNA Library Danio rerio cDNA 5', mRNA sequence.
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Identification and Characterization of Expressed Sequence Tags from
an Embryonic Zebrafish Heart cDNA Library
Unpublished (1999)
Contact: Liew CC
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kukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                               Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
WWW.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Hummain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/db_xref="taxon:7227"
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Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177228915
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40.2%; Pred. No. 58;
ative 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="BACN17E01"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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354 TATGAGGSAAAA 343
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       (bases 1 to 948)
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                                                                                                                                                                                                                     1064 GATAATCCGTCGAAGTCTGAGGATGGAAGGAAGGTGAAGGCTGTTCCTGAAAGGAATAAA 1123
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1 (bases) to (bases) to Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contect: Nori Satoh
Department of Zoology
                                                                                                                                                                             957
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                                                                                                                                                                                                                                       kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Nori Satoh unpublished cDNA library, tailbud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                838 TTACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCCATCATGGGTGAGATAGGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          898 CAATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTT
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                                                                                                    Length 831;
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                                                                                                 Score 35.4; DB 12; Length
Pred. No. 65;
0; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole animal"
/dev_stage="tailbud embryo"
/note="Vector: pBluescript SK"
116 c 133 g 173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Ciona intestinalis"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sākyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.2; DB Pred. No. 71; 0; Mismatches
                                                                                                                                                                                                                                                                               1124 AGTGACATCATGCCCTCTTTTTCTGGCTT 1152
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Best Local Similarity 52.3%;
Matches 78; Conservative
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Matches 73
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TITLE
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United valuations of the sequence of the sequence of submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                  Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACK48F19 of RPCI-98 library from Drosophila melanogaster (fruit
ALO/8714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      995 МНММИМИМИМТІНАКНІТІТНІТІТУММАМСМІТНІММИМИМИМИМАМИМССИСИСИМ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 THMCCCMMMMMMMMMMMMMMMMMMMMMTTTTTTTHWMMMMTT
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                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Drosophila melanogaster"
/db_xref="taxon:727"
/clone="BACR48P19"
/clone=1bb-"RPCI-98"
/note="end: TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.0%; Score 35.2; DF
15.4%; Pred. No. 76;
ative 125; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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555 ATTGTGAGATGCTGGT
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Gm-c1016-7678 5' similar to SW:SUSY_SOYBN P13708 SUCROSE SYNTHASE
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                                                                   AW509231.1 GI:7147309
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Best Local Similarity 55.9%
Matches 66; Conservative
                            mRNA sequence.
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                                                                                                                       soybean.
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BQ611687/c
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ORIGIN
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Niff.WGC_77"
/lab_host="Niff.WGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="Organ: lung; Vector: pbNR-LiB (Clontech); Site_1:
Sfii (ggocgctcggcc); Site_2: Sfii (ggocgttatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGATGGCC-3' and 3' Adaptor sequence:
5'-ATTCTAGAGGCCGACATGATGGCC-3' and 3' Adaptor
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb): 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS AW509231 43.2 bp mRNA linear EST 03-DEC-2001 DEFINITION sh92h11.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
                                                                                                                                                                 BG538455 861 bp mRNA linear EST 03-APR-2001
602567161Fl NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4691799 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 TTCCGGTCGGGATAAAAATCGCGCAGTGCGGTCCATGCAGACACATCCCCCACGGG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-refamilinih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCMISII row: i column: 16
High quality sequence stop: 433.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 861)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 12; Length 861;
Pred. No. 85;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .861
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4691799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 TCACGTGTCCATGCTCGAGCCGGATGC 447
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                                                                                                                                                                                                                  mRNA sequence.
BG538455
BG538455.1 GI:13530688
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Best Local Similarity 52.4%;
Matches 77; Conservative (
                                       | :::
755 CMCMMM 750
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
              CGGAAC 739
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                734
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AW509231/c
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BG538455/c
LOCUS
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                                                                                                                                                                                             DEFINITION
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JOURNAL
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Anote="Vector: palescript II XR; Site_I: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI: XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XLIO-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1037 Std Error: 0.00
Seq primer: -40RP from Glbco
High quality sequence stop: 431.
Location/Qualifiers
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kuaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                          Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Mitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Dipublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 GACGCTTCAGCCAGTACCATACCAAACGGTTCATTTTCCGAAGGCATGACCACCACAC 504
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-7678"
/clone=lib="Gm-c1016"
/tissue_type="immature flowers of field grown plants"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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55.9%; Pred. No. 89;
:ive 0; Mismatches 52;
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us-09-674-277-2.rst

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Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCORI adapters (5'0H-NATTCGGCACGAG and 3'GCCGTGGTCD) were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the ECORI XhoI restriction sites of the palluescript vector. The vector was previously dephosphorylated. The ligated cDNA fragments were transformed into DHIOB by electroporation. Library is in LB medium with ampicillin and glycerol 8%. Average insert size: 800 bp.
                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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  EST 26-JUN-2002
                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"vector: pBluescript II SK+; Site_I: EcoRI; Site_2: XhoI; The mRNA was prepared using polyatract mRNA system from PROMEGA. The CDNA was prepared using the STRATAGENE Kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI
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BQ611687 applear EST 26-JUN-200 sap63g01.y1 Gm-c1087 Glycine max cDNa clone SOYBEAN CLONE ID: Gm-c1087-5306 5' similar to SW:SUSY_SOYBN P13708 SUCROSE SYNTHASE
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1087-5306"
/tlssuc_type="Roots"
/lab_host="Bollo8"
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55.9%; Pred. No. 89;
ive 0; Mismatches
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Location/Qualifiers
                                                                                                                             BQ611687.1 GI:21601356
                                                                                                                                                                                                                                                                                                                                         (bases 1 to 445)
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BQ611687
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Matches
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/urganism="Glycine max"
/db_xref="taxon:3847"
/db_xref="taxon:3847"
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/tissue_type="Immature flowers of field grown plants"
/lab_host="x10-Gold"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
Xhoi; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XLIO-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-436 or contact via email: ccu@resgen.com
Insert Length: 1002
Seq primer: -40RP from Gibco
High quality sequence stop: 409.
                         sh89c12.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-7343 5' similar to TR:024302 024302 SUCROSE SYNTHASE ;, AW459606
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Shoemaker,R., Kehn,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptco,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Kitter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,P., Waterston,R. and Wilson,R.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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Pred. No. 89;
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ilarity 55.9%;
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//note-*Vector: pBluescript II XR; Site 1: ECORI; Site_2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
[GAGAGAGAGAGAGACAACTACTCCAGG(T)-18]. After
second-strand synthesis, the cDNA ends were 'polished'
with clone Ptu DNA polymerase, ligated to EcoRi adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 500bp cutoff, using GibcoREL Life
Technologies' cDNA Size Fractionation column. The column
Teluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+) that had been
digested with EcoRI and XhoI, and phosphorylated). Both
the white and blue colonies appear to contain recombinant
plasmids with cDNA inserts. Blue colonies 9n-15) have been
sequenced, and possess putative cDNA inserts. This library
was constructed by Dr. Paul Kelm & Virginia H. Coryell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna A., Bollan, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Waterston, R., 
                                                                           A1496532 478 bp mRNA linear EST 30-NOV-2001 sbl3a03.yl Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1004-8645 5' similar to SW:SUSY_PHAAU Q01390 SUCROSE SYNTHASE
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand This clone is
available through: ResGen, Invitrogen Corp. 2130 South Memorial
parkway Huntsville, AL 35801 For further information call: (800
)-533-4363 or contact via email: ccueresgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 1
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/clone_lib="Gm-cl004"
/tissue_type="root"
/lab_host="XL10-Gold"
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Public Soybean EST Project
Washington University School of Medicine
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/organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                        AI496532.1 GI:4397535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                          soybean.
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RESULT 40
AI496532/C
                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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FEATURES

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/note—"Vector: pBluescript II XR; Site_I: ECORI; Site_2:
XhoI; This CDNA library was constructed from mRNA isolated
from 'Desloy 5710' seedling roots. Tissue was taken from
7-day-old seedlings that had been propagated on paper
towels with distilled water. Tissue was taken from the tip,
to the first lateral root, usually about 3cm from the tip,
and flash-frozen in liquid nitrogen. Stratagene's cDNA
Synthesis Kit (catalog number 200401) was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: estewatson wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccuéresgen.com
Insert Length: 838 Std Error: 0.00
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW620859 507 bp mRNA linear EST 03-DEC-2001 sj47ell.yl Gm-c1033 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1033-453 5' similar to SW:SUSY_SOYBN P13708 SUCROSE SYNTHASE ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Department of Biology, Box5640, Northern Arizona University, Flagstaff, Az 86011, Phone: 520-523-1078 (Dr. 9aul Kaim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                            387 TTCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 IGCACAAIGAICICAGCAGCACCACCATIGCAIGIGGGGAAIGIIGGCAAGCCGCAAGIC 283
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1033-453"
/clone_lib="Gm-c1033"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                          Length 478;
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Public Soybean EST Project
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                                                                                                                                                                                                                                                                                          2.9%; Score 34.8; DE 55.9%; Pred. No. 90; Live 0; Mismatches
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Best Local Similarity 55.99
Matches 66; Conservative
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AW620859
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 512)
Maharas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ785148 512 bp DNA linear GSS 03-AUG-1999 HS_3159_A1_B06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3159 Col=11 Row=C, DNA sequence.
AQ785148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 ITCTGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACT 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3159 row: C column: 11
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 GACGCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACAC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 ATGGCCTCAACCACTGTCAAACCACAAAGCCTCGTATACAGCAGGCTGCAAAAGCAC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34.8; DB 10; Length 507;
Pred. No. 91;
0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ785148.1 GI:5692772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.9%;
Best Local Similarity 55.9%;
Matches 66; Conservative
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ORIGIN
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KEYWORDS
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library avallability, please contact Pieter de Jong
(Pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1031 row: I column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HS_5455_A2_E02_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1031 Col=4 Row=I, DNA sequence.
AQ662456
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 514)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
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                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="plate=3159 Col=11 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                          /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                          900 ATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                  Length 512;
                                                                                                                                                                                                                                                           11 others
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/db_xref="taxon:9606"
/clone="Plate=1031 Col=4 Row=I"
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                                                                                                                                                                                                                                                           133 t
                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 34.8; DE Best Local Similarity 52.0%; Pred. No. 91; Matches 78; Conservative 0; Mismatches
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                   High quality sequence stop: 512. Location/Qualiflers
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BAC ends
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DEFINITION
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MEDLINE
COMMENT
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AQ662456
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KEYWORDS
SOURCE
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ORIGIN
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AW279073/c
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-435 or contact via email: ccuéresgen.com
High quality sequence stop: 485.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, T., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
                                                                  donor
                                                                                                                                                                                                                                                                                                                                                                                                        960 IGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE440931 523 bp mRNA linear EST 04-DEC-2001 sp49g12.yl Gm-c1043 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1043-1631 5' similar to SW:SUSY_SOYBN P13708 SUCROSE SYNTHASE
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                                   /note-"Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"
                                                                                                                                                                                                                                                                                                                  900 ATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/db_xref="taxon:384"
/clone="GENONE SYSTEMS CLONE ID: Gm-c1043-1631"
/clone_lib="Gm-c1043"
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                                                                                                                                                                                                                             Length 514;
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                          4 others
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Pred. No. 91;
0; Mismatches
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BE440931.1 GI:9440426
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                       /sex="male
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Matches 78; Conserv
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BE440931/c
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JOURNAL
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KEYWORDS
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germinated for three days of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The ECORI-NotI restriction site of the pT773-Pac vector. The ligated cDNA fragments were directionally cloned into the ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoemaker, R., Kelim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Waylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public Soybean EST Project
Unpublished (1999)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/note="Vector: pSPORT1 (Life Technologies); Site_1: Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 ATGGCCTCAACCACTGTCAAACCAAAAGCCTCGTATACAGCAGGCTGCACGAAAGCAC 111
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Amenorial Parkway Huntsville, AL 35801 For further informs
call: (800)-533-433 or contact via email: ccueresgen.com
Insert Length: 329 Std Error: 0.00
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4444 Forest Park Parkway, Box 8501; St. Louis, MO 63108,
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1019-4940"
/clone_lib="Gm-c1019"
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Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.8; DB Pred. No. 91; 0; Mismatches
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Fax: 314 286 1810
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(Shoemaker,R., Kefa,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Glbbons,M., Pape,D., Harvey,N., Schurk,R., R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

To mpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
                                                  greenhouse grown plants. The library was prepared using greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript CDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the bluut-ended cDNA fragments were followed by Not I digestion. The CDNA fragments were directionally cloned into the Not I -Sal I restriction site of the pSPORTI vector. The ligated CDNA fragments were transformed into E. coli ElectroWax DH10B host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
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Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 420.
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constructed from mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 TGCACAATGATCTCAGCAGGACCACCATTGCATGTGGGGAATGTTGGCAAGCCGCAAGTC 161
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Site_2: Sal I; This cDNA library was constructed fisolated from immature seed coats (200–300 mgs) of
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/lab_host="DH10B"
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Pred. No. 91
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BM092322.1 GI:17021288
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xhoi; The cDNA library was constructed from mRNA isolated from very young seeds (less than 20mgs). The library was prepared using the Stratagene pBluescript II SK (+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an Xho I restriction site. Eco RI adaptors were ligated to the blunt-ended cDNA fragments followed by Xho I digestion. The cDNA insert is protected from Xho I digestion via methylation during first strand cDNA sythesis. The cDNA fragments were directionally cloned into the Eco RI-Xho Irestriction site of the pBluescript vector. The ligated cDNA fragments were transformed into Ecoli ElectroMax DH10B host cell. The library was constructed by Anu Khanna (Lila Vodkin lab, University of Illinois)."
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ID: Gm-c1049-4322 5' similar to SW:SUSY_SOYBN P13708 SUCROSE
B1427174
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/db_xref="taxon:3847"
/db_xref="Texon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1049-4322"
/clone_lib="Gm-c1049"
/tissue_lib="whole seedlings of greenhouse grown plants"
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Pred. No. 91;
0; Mismatches
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                                    /note="Vector: pBluescript II SK+; Site 1: ECORI; Site 2: XhOI; The Clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The CDNA library was constructed from mRNA isolated from whole seedlings of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site and 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhOI restriction site of the pBluescript vector. The ligated CDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizon University."
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ID: Gm-c1080-558 5' similar to SW:SUSY_SOYBN P13708 SUCROSE
SYNTHASE; mRNA sequence.
B1427022.
B1427022.1 GI:15204254
ESST.
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccueresgen.com
High quality sequence stop: 391.
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Warayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1080-558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 542;
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/dev_stage="3 week old"
/lab_host="DH10B"
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55.9%;
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Best Local Similarity 55.99
Matches 66; Conservative
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the tissue. The roots were missarinoses in thighton nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesis the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was henimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGACACACACTCCCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcosI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, KNase., DNAse-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (40V/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500Pp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Blotech) in a 2-mm diameter column and a bed volume of approximately lm. The column eluent was precipitated, redissolved, and ligated into Stratagene's please that
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
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                                                                                                                                                         Anote="Vector: pBluescript II SR+; Site_1: EcoRI; Site_2: AhoI; The mRNA was isolated from roots of 8 day old "Bragg' supernodulating mutant NRS382 seedlings that were infected with Bradyhizoblum japonicum, strain USDA 110, 72 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constucted in the laboratory of Dr. Paul Kelm and Dr. Virginia H. Coryell at Northern Arizona University."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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55.9%; Pred. No. 92;
iive 0; Mismatches
/tissue_type="Roots of 8
mutant NTS382 seedlings"
/dev_stage="8 days old"
/lab_host="DH10B"
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//decenvole="Vactor: paluescript II SR+; Site_I: ECORI; Site_2: Ahol; The mRNA was isolated from roots of bulked Minsoy x Noir RI progeny that are phenotypically susceptible to flooding damage. The plants were flooded (submerged) for 24 hours prior to harvest. Dr. Tara VanToal generoually provided the isolated mRNA. The roots were flash- frozen in liquid nitrogen. Stratagene's cDNA synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to ECORI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase., DNase-free water. The XhoI she within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (400/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff or a 2-mm diameter column and a bed volume of subsequence of the stract column and a bed volume of
                                                                                                                                                                                                                                                                       Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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K., Waterston, R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
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                                                                                                                        Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University Stopeol of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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High quality sequence stop: 426.
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314 286 1810 '
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/note="Vector: pBluescript II SK+; Site_1: ECORI; Site_2:
XhOI; The mRNA was isolated from roots of bulked Minsoy x
NoIf RI progeny that are phenotypically susceptible to
flooding damage. The plants were flooded (submerged) for
24 hours prior to harvest. Dr. Tara Vanfoal generously
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in liquid nitrogen. Stratagene's cDNA Synthesize the CDNA.
First-strand synthesis was used to synthesize the CDNA.
First-strand synthesis was berformed with 5 methyl dCTP,
hence the ligated CDNA was hemimethylated. A modification
of Stratagene's first-strand synthesis primer was used. An
anchor' nucleotide (V=A, C, or G) was added to the 3' end
of the primer at the 5' end of the poly(A) tract.
After second-strand synthesis, the CDNA ends were filled
in with cloned Pfu DNA, ligated to ECONI adapters and
subsequently phosphorylated. The CDNA was then
precipitated and redissolved in sterile, RNase.,
DNasse-free water. The XhOI site within the first- strand
synthesis primer was then restricted by digestion with
XhOI from Promega (400/ul); all XhOI sites in the CDNA
would be protected by their hemimethylated status. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com Seq primer: -40RP from Gloco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA constructs were size-fractionated with a 500bp cutoff , using Sephacryl S-500 High Resolution (Pharmacia Biotech ) in a 2-mm diameter column and a bed volume of
                                                                       BI787127 584 bp mRNA linear EST 29-NOV-2001 sag71f10.yl Gm-c1082 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1082-2179 5' similar to SW:SUSY_SOYBN P13708 SUCROSE
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Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/lab_host="DH10B"
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    No. is the number of results predicted by
re greater than or equal to the score of the
is derived by analysis of the total score di

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1 US-09-103-840A-1

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1 US-09-103-60-6

1 US-09-103-60-7

1 US-09-103-558-1

1 US-09-103-558-1

1 US-09-103-558-1

1 US-09-103-558-1

1 US-09-370-700-1

1 US-08-961-527-155

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Maximum Match 100%
Listing first 150 summaries
                                                                      nucleic search, using sw model
                                                                                                   June 18, 2003, 02:08:24
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Score 57.2; DB 4; Pred. No. 1.1e-06; 0; Mismatches 98;

Length 4403765;

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2447373 ITCICGGCGGCGGCGCCCATCGCGGCCCGATCCCGATCGATCAGCAGCACACACGCCAC 2447432
                                                                                                                                                                                                                                                                                                    332 IGCGCCGGTCCAIGCAGACACATCCCCCACGGGIAACAGCGTCCCTGTCACATICTTCIG 391
                                  FEATURE:
COTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                            TTCTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAAATCGCGCAG
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                 4.8%;
illarity 54.2%;
Conservative 0
                                                                                                                                                                       Best Local Similarity
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US-09-103-840A-1
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Sequence 2, Sequence 2, Application US/09103840A
Sequence 2, Sequence 2, Application US/09103840A
SPECANT: PELSICHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 24566-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: PATENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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Sequence 42
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Sequence 8
Sequence 2
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US-08-611-107-32

US-08-611-107-32

US-08-248-474-100

US-08-248-474-100

US-08-756-849-100

US-08-759-101-13

US-08-79-109-13

US-08-79-109-8

US-09-134-001C-2575

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US-08-615-192A-245
US-08-665-240-2
US-08-453-472-1
US-08-453-472-1
US-08-481-993B-42
US-08-484-993B-42
US-08-484-158B-42
US-08-484-158B-42
US-08-484-158B-42
US-08-484-158B-42
US-08-484-158B-42
US-08-444-144-2
US-08-449-253A-42
US-08-499-5
US-08-297-510-5
US-08-297-510-5
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US-08-247-901C-1
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US-09-426-436-1
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                                                           US-09-103-840A-2
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2450192 CACCGTTTCCGGCGCCTCCGCCAGAATTGCCGGCATTACCGGCACGCCGGCGGAGGC 2450251
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2450072 TTCTCGGCCGCCGCCCCATCGCGACGCCCCGATCCCATCGATCAGCAACTCGGCCAC 2450131
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                                                                                                                                                                                                                                                                      Sequence 1, Application US/09103840A
Sequence 1, Application US/09103840A
Sequence 1, Application US/09103840A
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 2456-20007.00
FILE REFRENCE: 2456-20007.00
CURRENT APPLICATION UNBER: US/09/103,840A
SOFTWARE: PALENTING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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54.2%; Pred. No. 1.1e-06;
ive 0; Mismatches 98; Indels 0;
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                                                                                                                      TICAGCCAGIACCAIACCAAACGCIICAIITICC 485
                                                                                    TTCAGCCAGTACCATACCAAACGCTTCATTTTCC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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Matches 116; Conservative
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ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 271,653
FILING DATE: 16-NOV-1988
APPLICATION NUMBER: 410,831
FILING DATE: 22-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: MURPHY, Cheryl
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 53.4
Matches 71; Conservative
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US-09-066-046-1/c
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                                                     GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
SOFTWARE: PATENT DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENT DATE: 1.386-24
SOFTWARE: PATENT DATE: 1.386-24
SOFTWARE: PATENT DATE: 1.386-24
SOFTWARE: PATENT DATE: 1.386-24
SOFTWARE: PATENT DATE: 1.386-24
SOFTWARE: PATENT DATE: 1.386-24
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
CTHER INFORMATION: represent a, t, c or g
GS-09-103-640A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FLEISCHAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
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50.8%; Pred. No. 0.65;
Live 0; Mismatches 92; Indels 0;
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Pred. No. 0.65;
0; Mismatches 92; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92; Indels
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; ORGANISM: Mycobacterium tuberculosis
; CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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                 Sequence 2, Application US/09103840A Patent No. 6294328
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Best Local Similarity 50.8%;
Matches 95; Conservative
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577809 CGAAACA 577803
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Best Local Similarity
Matches 95; Conserval
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US-09-103-840A-2/C
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GCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 CTTAAACCAGAGTTCATAAGCTTGATGAGTTATGATAAAAAGATGTTCATCATGGATTTT 226
                                                                                               393 ATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCT
                                                                                                                                             576487 ACCGCGACGGGCAGCCCGCCCACCGCGGGCCACCACCGTGTGCCGCACGCTTGGGCC
                                                                                                                                                                                                 453 TCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1013 ATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COMINGS, DAVID E.
TITLE OF INVENTION: TOURETTE SYNDROM, AUTISM AND ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: mone...
STOREY, James
STOREY, James
BELTZ, Gerald A.
COUGHLIN, Richard T.
TITLE OF INVENTION: CHARACTERIZATION OF GRANULOCYTIC
BIRLICHIA AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33.8; DB
Pred. No. 0.63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BEHAVIORS

NUMBER OF SEQUENCES: 5

CAPPLICATION DATA:

PILING DATE: 03-AUG-1990

PRIOR APPLICATION DATE: 125-AUG-1967

PRIOR APPLICATION DATE: 25-NOV-1967
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ORGANISM: Human
US-09-141-000-2
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Pred. No. 1.7;
0; Mismatches 100; Indels
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COUGHLIN, Richard T.
COUGHLIN, RICHARACTERIZATION OF GRANULOCYTIC
EHRLICHIA AND METHODS OF USE
                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:

NAME: SUPERFO, COlleen
REGISTRATION NUMBER: 39,850
REFREENCE/DOCKET NUMBER: 106.941.155
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                               APPLICATION NUMBER: US/09/066,046A FILING DATE: 24-Apr-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-066-046-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09066046A
Patent No. 6204252
GENERAL INFORMATION:
APPLICANT: MURPHY, Cheryl
STOREY, James
                                                                                                                                                                                                                                                                                                                                                LENGTH: 3147 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.8%;
Local Similarity 48.2%;
hes 93; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 65
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                             COMPUTER READABLE FORM:
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Matches
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733 GCGGAACATTGTCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGTAACGGTCGCATGG 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 CCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         947 GCACAATAATGGATGATTCTACTTGTACTGCAGTAGTGTTTACTTGGTTAACAACCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 5570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 4; Length 557;
Pred. No. 2.3;
0; Mismatches 100; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chen, Fang
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 19999Y
CURRENT APPLICATION NUMBER: US/09/141,000
CURRENT APPLICATION NUMBER: 30
CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2.0
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 2.8%; Score 32.6; DB 3;
1 Similarity 10.8%; Pred. No. 0.78;
43; Conservative 110; Mismatches 246;
                                                                                                                                                                                      REGISTRATION NUMBER: 39,850
REGISTRATION NUMBER: 39,850
REPERBRICE/DOCKET UNDERR: 106.941.155
TELECOMUNICATION INFORMATION:
TELEFRAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,046A
FILING DATE: 24-Apr-1998
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09141000 Patent No. 6054295
                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 5570 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Superko, Colleen
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%;
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Best Local Similarity
Matches 43; Conserva
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973 TGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTGTCATGGCCACTAT 1032
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                       913 GATAATICAGGGAAAACGTICIGGICTIACGGGIGATGIAGGITITITGICTGACAAIAG 972
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204 PAKKPLTKIVSYLLVAEPDKLYAMPPPGMPEGDIKALTTLCDLADRELVVIIGWAKHIPG 263
                                                                                                                                                                                                                                                                       793 CTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGAATAACCGTTACCGGTGTCCTGA 852
                                                                               353 CACCTTCCGCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACAATGAAATCACACA 912
                                                                                                                                                                                                                                                                                                                                                                   324 ILQLVRRYKKLKVEKEEFVTLKALALANSDSMYIEDLEAVQKLQDLLHEALQDYELSQRH 383
                                                                                                                                                                                                                                                                                                                                                                                                              1093 GAAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACAT 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 EEPWRTGKLLTTLPLLRQTAAKAVOHFYSVKLQGKVPMH 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Y. Tom
APPLICANT: Corley, well C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN SMN-LIKE PROTEIN
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
GTREET: 3174 Porter Dr.
GTYS: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0482 US
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Patent No. 6130064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650-855-05
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRSTNOT24
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; CLONE: 3769729
US-09-028-327-2
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859
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                                         Gaps
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     Length 2426;
                                      Indels
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:: Nelson, Randy
:: Smith, Michael
: Sequence of a Bovine Herpesvirus Type-1 etc.
                                                                                                                                                                                                                                                                                                                         APPLICANT: Letchworth, Geoffrey J.
APPLICANT: Israel, Barbara A.
TITLE OF INVENTION: HERPESVIRUS VACCINE AND METHOD
TITLE OF INVENTION: OF USING SAME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: coding sequence for gI glycoprotein LOCATION: 379 to 3165
IDENTIFICATION METHOD: sequence analysis
     DB 3;
%; Score 32.6; DI
%; Pred. No. 2;
. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: MICTOSOFT WORD 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/607,794
FILING DATE: 02-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: NICHOLAS J. SEAY
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96296910
TELEPHONE: (608)251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: bovine herpervirus-1 INDIVIDUAL ISOLATE: P8-2 strain
                                                                                                                                                                                                                                                                      Sequence 1, Application US/08035558
Patent No. 5462734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
CITY: MADISON
STARE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             Quarles and Brady
Similarity 54.6%;
5; Conservative . (
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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STRANDEDNESS: double
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Query Match
Best Local Simi
Matches 65;
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VOLUME: 1
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AUTHORS:
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Conservative 205;
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                                                                             Score 32.2; DB 1; Length 3519;
Pred. No. 3.3;
0; Mismatches 84; Indels 0
                                                                                                                                                                                                                                                           416 CTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGT 461
                                                                                                                                                                                                                                                                                    76 GITITCCACGCIAAAGIACAGCGCGGTGITTGGCGCTGCGCGAAGT 31
                                  1: FROM 379 TO 3165
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                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30472/114 IMMU FELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.7%; Score 32.2;
5.3%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                  RELEVANT RESIDUES IN SEQ ID NO: US-08-035-558-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foley & Lardner
                                                                             2.7%;
milarity 49.4%;
Conservative 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity
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                                                                                 Query Match
Best Local Similarity
       542-549
1988
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                                                              759 CAGGCGTGGATATGCAGGGGTAACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCG 818
                                                                                                                                                                                879 ATGGGTGAGATAGGCACAACAATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTC 938
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Mismatches 188; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/^^
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEV F.
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FR: 30472/114 IMMU
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
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APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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                                                                                                                                Length 7218;
                                                                                                                           Query Match 2.7%; Score 31.8; DB 1; Length 7 Best Local Similarity 3.8%; Pred. No. 6.8; Matches 15; Conservative 204; Mismatches 176; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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FILING DATE: 09-MAR-1998
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Crawford, Kathryn P.
Maddurl, Krishnamurthy
Merlo, Donald J.
Treadway, Patti J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Grawford, Kathryn P.
APPLICANT: Madduri, Krishnamur
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Waldron, Clive
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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STATE: Indiana
                                 TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Example Madduri, Kathryn P
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: 1999-08-09
CURRENT FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                              Length 80161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.4; DB 4; Length 80161; Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                            Query Match 2.7%; Score 31.4; DF
Best Local Similarity 56.2%; Pred. No. 37;
Matches 59; Conservative 0; Mismatches
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Patent No. 5744313
GENEZL INFORMATION:
APPLICANT: Williams, Lewis T.
NAME: Stuart, Donald R
REGISTRATION UNDBER: 28,479
REFERENCE/DOCKET NUMBER: 50,61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09370700 Patent No. 6274350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: US CERALIER FILLING DATE: 1998-03-09 NUMBER OF SEQ ID NOS: 39 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                     linear
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Matches 59; Conserv
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US-08-353-550-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-370-700-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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510 ccrrergaarcagagaccreccacarrergagarcrecgaaggerreccaaggarer 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3100 No. 6218162west Center, 90 South Seventh Street CITY: Minneapolis STATE: Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Krystal, Gerald
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MERCHANT & GOULD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFENCE/DOCKET NUMBER: M&G 7933.49-US-01
TELECOMMUNICATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                FILING DAILS.
CLASSIFICATION: 435
PRIOR APPLICATION DAIRS.
APPLICATION NUMBER: 08/353,550
FILING DAIE: 09-DEC-1994
ATTORNEY, AGGENT INFORMATION:
NAME: Murphy, MATCHEW B.
RECISTRATION NUMBER: P39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.2;
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FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
                                UMBER: US/08/551,687
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08664962B Patent No. 6218162 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 415-326-2400 TELEPRAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              LENGTH: 1425 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.6
Best Local Similarity 54.3
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-551-687-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 CACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAAC 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williams, Lewis T.
APPLICANT: Cavanaugh, William M.
TITLE OF INVENTION: No. 5925547el Protein Domain Which Binds
TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                     TITLE OF INVENTION: No. 5744313el Protein Domain Which Binds TITLE OF INVENTION: Tyrosine Phosphorylated Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                      E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,550
FILING DATE: 09-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B:
REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.2; DB
Pred. No. 4.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02307K-057300
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-551-687-7

; Sequence 7, Application US/08551687

; Patent No. 5925547

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.3%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
                                                                                                                                                                                                         ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One marries CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..1422
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; LOCATION: 1..1
US-08-353-550-7
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                                                                                                         ADDRESSEE:
                                                                                                                                                                                        COUNTRY:
                                                                                                                              STREET:
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468 CCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAAC 527
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                                                                        418 CACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAAC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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       DB 4; Length 3031;
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                                         Indels
                                                                                                                                                                                                                                                                                                 APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PACENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                                                        E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
     Score 31.2; DE
Pred. No. 6.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31.2; DE
Pred. No. 6.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: FP-LJ 1453
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: PCT/US95/03747
27-MAR-1995
                                                                                                                                                                                                                                                PCT-US95-03747-1/c; Sequence 1, Application PC/TUS9503747; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1904 GCTGGAAGCAGGGAAGGGGC 1885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.68;
     Query Match 2.6%;
Best Local Similarity 54.3%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3259 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.6
Best Local Similarity 51.4
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .CDS
112..2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27
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COMPUTER: IB
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US-08-896-449A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92122
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PCT-US95-03747-1
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                                                                                                                                                                                                                              Length 3031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09311743
Patent No. 6238903
GENERAL INFORMATION:
APPLICANT: KTYSTAL, Gerald
TITLE OF INVENTON: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SECUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7771-32
REFERENCE/DOCKET NUMBER: 7771-32
TELECOMMUNICATION INFORMATION:
TELEFA: 416-364-7311
TELEFA: 416-361-1398
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3031 base pairs
                                                                                                                                                                                                                            ; Score 31.2; DE
; Pred. No. 6.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/311,743 FILING DATE: 14-May-1999 CLASSIFICATION: classification: classification: classification: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : NAME/KEY: CDS
; LOCATION: 82..1503
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-311-743-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BERESKIN & PARR STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
TLE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          Query Match 2.6%;
Best Local Similarity 54.3%;
Matches 63; Conservative
LENGTH: 3031 base pairs
                                                                                                       ORGANISM: Homo sapiens
STRAIN: Shc Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto STATE: Ontario
                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 82..1503
US-08-664-962B-3
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7539 TCCTCCCAGAACTGGCCCACAGGGTAGATGGTGCT 7504
                      510 ATCCGGTAGACCGGTAACGCTGGGAAAAGGGCACCT 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-403-768-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 8802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-132-652-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 GCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Terrier is Caused by a Single Base Deletion in
Exon Four of the von Willebrand Factor Gene
Journal of the American Veterinary Medicine Association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 203..8641
OTHER INFORMATION: /function= "Blood Clotting Protein"
OTHER INFORMATION: /product= "Canine von Willebrand Factor"
OTHER INFORMATION: /standard_name= "vWF"
AUTHORS: Venta, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 8802;
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                                                           APPLICANT: Verta, Patrick J
APPLICANT: Yuzbasiyan-Gurkan, Vilma
APPLICANT: Schall, William D
APPLICANT: Schall, William D
APPLICANT: Brewer, George J
TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
TITLE OF INVENTION: FACTOR AND METHODS OF USE
CORRESPONDENCE ADDRESS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: 1996
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 8802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brewer, George J.
Von Willebrand's Disease in the Scottish
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     Harness, Dickey & Pierce, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%; Score 31.2; Di
50.0%; Pred. No. 12;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Smith, Deann F.
REFERENCE/DOCKET NUMBER: 2115-001226
TELECOMMUNICATION INFORMATION:
TELEPHONE: 248-641-1600
TELEFA: 248-641-0270
TELEX: 297637
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8802 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/896,449A FILING DATE: 18-JUL-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: L1, Jianping AUTHORS: Yuzbasiyan-Gurkan, Vilma AUTHORS: Schall, William D. AUTHORS: Brewer
Sequence 1, Application US/08896449A Patent No. 6040143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                      5445 Corporate Drive
                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 50.0
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exon Four
                                                                                                                                                                                                                                                                                                Michigan
                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 48098
                                                                                                                                                                                                                                                  STREET: 544:
                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                STATE:
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APPLICANT: Lam, Joseph S.
APPLICANT: Lam, Joseph S.
APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori L.
APPLICANT: Burrows, Lori L.
APPLICANT: Walsh, Andrew
APPLICANT: Walsh, Andrew
TITLE OF INVENTION: No. 6444804el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: No. 644804el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: NOWBER: US,099/403,768
CURRENT APPLICATION NUMBER: US,00/045,418
PRIOR PILING DATE: 1997-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 TGAATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCCACGCCGGAGACTGAC 449
                                                 GENERAL INFORMATION:
APPLICANT: Venta, Patrick J
APPLICANT: Yuzbasiyan-Gurkan, Vilma
APPLICANT: Yuzbasiyan-Gurkan, Vilma
APPLICANT: Schall, William D
APPLICANT: Brewer, George J
APPLICANT: Duffendeck, John
TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 2115S-001226CPB
CURRENT APPLICATION NUMBER: US/09/132,652
CURRENT APPLICATION NUMBER: US/09/132,652
ERRLIER APPLICATION NUMBER: US/09/149
ERRLIER PILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 GCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCA
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1997-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09403768 Patent No. 6444804
; Sequence 1, Application US/09132652; Patent No. 6074832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.6%;
Best Local Similarity 50.0%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7 PATENTIN Ver. 2.0
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96-296-2185-2
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Mangelsdorf, David J.
Haussler, Mark R.
Pike, J. W.
Shine, John
                                                                                                                                                                                                                                                                                         Sequence 5, Aplication US/07737736B Patent No. 5260199 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
REFRENCE/DOCKET NUMBER: 96-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 414-277-5715
TELEFAX: 414-277-5774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McDonnell, Donald P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                    5781 GGATAGATTTCACC 5794
                                                                                                                                                531 GGGAAAGGGCACC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker, Andrew R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1399 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                        US-07-737-736B-5/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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Sequence 155, Application US/08961527

Patent No. 6420135

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5601 ACATCTTCCTTCTCAAATAAAATCCATCAACCCTATGTTCAATAATTTCACTTAACCCG 5660
                                                                                                                                                                                  363 GGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCCGGCCCGTCTCACTG 422
                                                                                                                                                                                                                                                                    423 GCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 CCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCA 470
                                                                                                                                                                                                                           956 GGCAGCACCCGCCCGGCGTCGGCCTCGGCGATGTGGGCCATAGCCGCAGACATCGGTC 897
                                                                                                                                                                                                                                                                                                             896 ACCAACACCGGCAGGCCGGAGACCAGCGCCTCCAGCAGCACCGTACCGGTGTTCTCGTTG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 ACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTGTGAATGACATCAGGGATCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                Gaps
                 OTHER INFORMATION: Description of Organism: Pseudomonas aeruginosa; OTHER INFORMATION: serotype 05 strain PAO1 US-09-403-768-7
                                                                                                   Query Match

2.6%; Score 30.8; DB 4; Length 1122;
Best Local Similarity 50.7%; Pred. No. 4.9;
Matches 74; Conservative 0; Mismatches 72; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30.8; DB 4; Length 6 Pred. No. 14; 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
.COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                    483 TCCGAAGGCATGACCACCACACTGGC 508
                                                                                                                                                                                                                                                                                                                                                                                          836 TAGGCCGGGTGGATCAGCAGGTCGGC 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.6%;
Best Local Similarity 47.4%;
Matches 92; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ROCKYILL STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20850
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US-08-961-527-155
FEATURE
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471 AACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCT
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APPLICANT: Ross, Troy K.
APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
NUMBER OF SOURNESS: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: O'Malley, Bert W.
TITLE: Cloning and expression of full-length cDNA
TITLE: encoding human vitamin D receptor
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,736B
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Score 30.4; DB 4; Length 780; Pred. No. 5.4; 0; Mismatches 31; Indels

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323 ATCGCGCAGTGCGGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCAC 382
                                                                                                                                                                           383 ATTCTTCTGAATGACATCAG 402
                                                                                                                                                                                                                                                         231 CTTATTAACACTGACATCGG 212
                                                                                  Query Match 2.6%;
Best Local Similarity 61.2%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Conservative
                          ) ORGANISM: Escherichia coli
US-09-650-855-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Best Local Similarity
Matches 85; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-08-682-847-1
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                                                                                                                                                                                                                                                                                                                                        RESULT 27
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Sequence 26, Application US/09650855
Sequence 26, Application US/09650855
Sequence 26, Application US/09650855
SERENT NO. 6365355
GENERAL INFORMATION:
APPLICANT: MACUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA TITLE OF INVENTION: MISMATCHES
FILE REFERENCE: IL-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR FILING DATE: 2000-08-29
PRIOR FILING DATE: 2000-03-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 ATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCAC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09651656
Sequence 26, Application US/09651656
GENERAL INFORMATION:
APPLICANT: MCGUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERNORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
TITLE OF INVENTION: DNA DAMAGE AND. DNA MISMARCHES
FILE REFERENCE: IL-10689
CURRENT PELLING NATE: 2000-08-29
PRIOR PELLING DATE: 2000-08-29
PRIOR PELLING DATE: 2000-03-28
MINARED OF SEO. TO MAC. 106
                                                                                                        694 GTCCTITITCGGGACGIAGCATCCCCACCTGAACGAIAAGCGGAACATIGTCTGCTGATG 753
                                                                                                                                                                                 754 CAGCCCAGGCGTGGATATGCAGGGGTAACGGTCGCATGGCTTCATTATGCAATGCGGGCC 813
                                                                                                                                                                                                         0; Gaps
                                                                        Gaps
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                                ; DB 1; Length 1399;
5.5;
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                                                                      Indels
                                                                      59;
                                  Score 30.6; DB
Pred. No. 6.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 ATTCTTCTGAATGACATCAG 402
                                  Query Match 2.6%;
Best Local Similarity 52.8%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Escherichia coli
US-09-651-656-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                 814 AGTCG 818
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US-09-651-656-26/c
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LENGTH: 780
US-07-737-736B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.6%; Score 30.4; DB 2; Length 3382; 48.3%; Pred. No. 13; ative 0; Mismatches 91; Indels 0;
                                                                                        APPLICANT: BABLUK, LORNE
APPLICANT: BABLUK, LORNE
APPLICANT: VAN DEN HURK, SYLVIA
APPLICANT: ZAMB, TIM
APPLICANT: TIZZATRICK, DAVID
TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,847
FILING DATE: 12-JUL-1996
CLASSIFICATION: 536
ATTORNEY/AGBNT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REGISTRATION NUMBER: 35,636
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
US-08-682-847-1/c; Sequence 1, Application US/08682847; Patent No. 5858989
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 706141'
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3382 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 813-5600
(415) 494-0792
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2057 TGCAGCCCCACCGGATCGCCCAGGTCCACGCCAACGCCGCCGCTACGCCGCCGACCACG 2116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 TCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGT
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing Same
TITLE OF INVENTION: Mutasynthesis
                                                                                                                                                                                                                                                                         Length 2888;
                                                                                                                                                                                                                                                                                                               Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CLTY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                             Mismatches 118;
                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, De
                                                                                                                                                                                                                                                                       Score 30.2; 1
Pred. No. 13;
                                                    FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2888
                                                                                                                                                                                                         ; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                     2.6%;
ilarity 46.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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COUNTRY: United States
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                           101;
                                                                                                                                                                                           TYPE: DNA
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Best Local 9
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                                            CGCCCCACCCGCCCCCCGCGCCCCAGCATAAACGCGGCCAGCTCCTTGAGGTGCGG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                    APPLICANT: COUZET, Joel
APPLICANT: BARRIERE, Jean-claude
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: DEBUSCHE, Laurent
APPLICANT: FAMECHON, Alain
APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 4.2;
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APPLICANT: BLANC, Veronique
APPLICANT: THIBAQT, Denis
APPLICANT: BAMAS-JACQUES, Nathalle
APPLICANT: BLANCHE, Francis
                                                                                                                                                                                                                                                                                                   THIBAUT, Denis
BAWAS-JACQUES, Nathalie
BLANCHE, Francis
COUZET, Joel
                                                                                                                                                                                                                               Sequence 4, Application US/08765907A
Patent No. 6352839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08765907A Patent No. 6352839
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DEBUSSCHE, Laurent
FAMECHON, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.6%;
Best Local Similarity 46.1%;
Matches 101; Conservative
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: BLANC, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUZET, Joel
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US-08-765-907A-4
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LENGTH: 387
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APPLICANT:
APPLICANT:
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APPLICANT:
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TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                             Query Match 2.5%;
Best Local Similarity 46.6%;
Matches 95; Conservative (
        ORGANISM: Homo saplens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Conklin, Darrell
APPLICANT: Yamamoto, Gayle
                                                                                             1..4342
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                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-482-180A-3
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PCT-US94-05277-1
                                                              FEATURE
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                                                                                                                                                                                                                                                   333 GCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGA 392
                                                                                                                                                                                                                                                                                                                     393 ATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCT 452
                                                                                                                                                                                    273 TCTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAGT 332
                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Johnson, Karen
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Vogelstein, Bert
APPLICANT: Zabrecky, James R.
TITLE OF INVENTION: Antibodies Specific for DCC Gene Product
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
                                                                                                                  DB 4; Length 4608;
                                                                                                                  Score 29.6; DB 4; Length 4
Pred. No. 28;
0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Banner, Birch, McKie & Beckett
1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42709
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202,508.9100
                                                                                                                                                                                                                                                                                                                                                                                                               453 TCAGCCAGTACCATACCAAACGCT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9405277 GENERAL INFORMATION:
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruskin, Arthur
Jarosz, David E.
                                                                                                                  Query Match
Best Local Similarity 46.6%;
Matches 95; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4608 base pairs
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TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                NAME/KEY: CDS
LOCATION: 1..4342
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                    ; LOCATION:
US-09-041-886-24
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559 CICCGCICATICCCAGGIGITCIGICIGCIGACGCAGACGIGCIICGIATICIICACGCC 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 ATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCT 452
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                                                                                                                            Gaps
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Length 4608;
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Best Local Similarity 21.7%; Pred. No. 14;
Matches 66; Conservative 53; Mismatches 185; Indels
      Score 29.6; DB 5; Length 46 Pred. No. 28; 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Jaspers, Stephen
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
TITLE OF INVENTION: BETA-1,3-GALACTOSILTRANSFE
FILE REFERENCE: 98-80
CURRENT PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/115,721
PRIOR PILING DATE: 1999-01-12
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COTHER INFORMATION: n is any nucleotide correction in some control in its and nucleotide correction in its and nucleotide correction in its and nucleotide correction in its angle of the 
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Patent No. 6361985
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679 GCAGCATAAATTCATGTCCTTTTTCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAA 738
                                                                                                                                                                                                                                                440 GGGCNMGNGGNMGNCARYTNAARYTNGTNTTYYTNYTNGGNGTNGCNGGNWSNGCNC 499
260 TNWSNYTNCCNWSNMGNCAYMGNYTNTTYYTNACNTAYMGNCAYTGYMGNAAYTTYWSNA 319
                                                                                   320 THYTNYTNGARCCNWSNGGNTGYWSNAARGAYACNTTYYTNYTNYTNGCNATHAARWSNC 379
                                                                                                                              CATTGTCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGGTAACGGTCGCATGGCTTCAT 798
                                                                                                                                                                                                                  199 TATGCAATGCGGGCCAGTCGAAACCCGGTGGAATAACCGTTACCGGTGTCCTGACACCTT 858
                                                                                                                                                                         380 ARCCNGGNCAYGINGARMGNMGNGCNGCNATHMGNWSNACNTGGGGGNMGNGINGGNGGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATER: PROFINER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: CUSHWAN DARBY & CUSHWAN
SEE: Intellectual Property Group of
SEE: Pillsbury Madison & Sutro LLP
... 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GUAN, HANDING
TITLE OF INVENTION: MODIFICATION OF STARCH
TITLE OF INVENTION: SYNTHESIS IN PLANTS
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Paul N. Kokulis
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 222957/1.02.15C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPRA: (202) 861-3000
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572,951
FILING DATE: 15-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,602
FILING DATE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ... 800
CLASSIFICATION: 800
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/263,921
FILING DATE: 21-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08572951
Patent No. 5824790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEELING, PETER L.
KNIGHT, MARY E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-JUN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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EDNESS: both
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                                                                                                                                                                                                                                                                                                      859 CCGC 862
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2.5%; Score 29.2; DB 1; Length 2380;

Query Match

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1686 YTGNACRTCYTGNCCNGCDAT-----CCARTGDAINGCRTCNGCDAIDAIRICNACNCC 1633
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                                                                                                                                                 517
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                                                                   398 ATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGC
                                                                                                                                               458 CAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTA
                                                                                                                                                                         518 GACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGGTCATTCCCAGGTG
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                                                                                                                                                                                                                                                                                                 578 ITCTGTCTGCTGACGCAGACGTGCTTCGTATTCTTCACGCCCGGCGCCCACCACGAGCCA
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                                   Gaps
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Sequence 48, 407681
GENERAL INFORMATION:
APPLICANT: Glordano, Antonio
APPLICANT: Baldi, Alphonso
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
TITLE OF INVENTION: OF CANCER
NUMBER OF SEQUENCES: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. Suite 1800 Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
                                 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Monaco, Daniel A
REGISTATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8121-13 US1
RELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELERAX: (215) 568-8383
INFORMATION FOR SEQ ID NO: 48:
                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1572 NCCNARYTGNCKYTGNARNG 1553
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28.98; Pie
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-832-883-48
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                             Conservative
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, G
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           Best Local Similarity
Matches 110; Conserv
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1056 GCTAGACCAG 1047
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                                                RESULT 36
US-09-293-505-8
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Best Local S.
Matches 46
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                                                                                                             1176 TGAACTCAGGTGATTCGCCTGCCTCAGCTCATAAAAGTGCTGGGATTACAGGCGTGAGC 1117
                                                                                                                                                             394 TGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTT
                                                                               394 TGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTT
                                                     Gaps
                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/08832877
Patent No. 5840506
GENERAL INFORMATION:
APPLICART: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: SLILE 1800 TWO Penn Center Plaza
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                   Length 3865;
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                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                       DB 1;
                   Score 29.2; DB; Pred. No. 34; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29.2; DE Fred. No. 34; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US2
RELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 3865 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic) US-08-832-877-48
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Best Local Similarity 51.5%;
Matches 67; Conservative
                     Query Match 2.5%;
Best Local Similarity 51.5%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                             US-08-832-877-48/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Ph.
STATE: P.
COUNTRY:
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1073 TCGAAGTCTGAGGATGGAAGGAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACATC 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 CITAAACCAGAGTICAIAAGCITGAIGAGTIAIGAIAAAAGAIGTICAICAIGAITII 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 CCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCA 470
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5405943-1/c
;PATENT NO. 5405943
APPLICANT: COMINGS, DAVID E.
; TITLE OF INVENTION: TOURETTE SYNDROM, AUTISM AND ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 6; Length 748;
Pred. No. 15;
0; Mismatches 65; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29.2; DB 4;
Pred. No. 35;
0; Mismatches 28;
Sequence 8, Application US/09293505; Sequence 8, Application US/09293505; Patent No. 6348775; GENERAL INFORMATION:
APPLICANT de Sauvage, Frederic; APPLICANT de Sauvage, Frederic; APPLICANT de Sauvage, Patched-2; TILLE OF INVENTION: Patched-2; FILE REFERENCE: 14405R1; CURRENT FILING DATE: 1999-04-15; CURRENT FILING DATE: 1999-04-15; NUMBER OF SEQ ID NOS: 32; SEQ ID NO 8; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/562,596
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 125,577
FILING DATE: 25-NOV-1987
APPLICATION NUMBER: 271,653
FILING DATE: 16-NOV-1988
APPLICATION NUMBER: 410,831
FILING DATE: 22-SEP-1989
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Best Local Similarity 51.1%;
Matches 68; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3637 AACACATATTGTTC 3650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 2.5%;
1 Similarity 62.2%;
46; Conservative
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US-09-293-505-8
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173 GAGGATCCGCCGTTATCTGTTGCATTTCCCCTTAGCCTGACTAGCCAGAGACACAATGAT 232
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Burland, Valerie
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                    COMPUTER ERADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.5%; Score 29; DB 4 Best Local Similarity 55.4%; Pred. No. 48; Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/110,955
                                                                                                      COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:-
FILING DATE:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: BTOOKSE, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/POCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-453-702B-39/c; Sequence 39, Application US/09453702B Patent No. 6365733; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 309-8504
TELERAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 5338 base pairs
                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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Maryland
: USA
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                                        20850
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US-08-961-527-50
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Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 GAGGATCCGCCGTTATCTGTTGCATTTCCCCTTAGCCTGACTAGCCAGAGACACAATGAT 232
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                     APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
UNDER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                  US-08-858-207A-78/c
; Sequence 78, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P50475
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APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.58;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                            Hodgson, John
Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.5
Best Local Similarity 55.4
Matches 56; Conservative
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                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             STATE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Vladimir Shamanin
APPLICANT: Ethel Michele De Villiers
APPLICANT: Zur Hausen
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/578,634
ATTORNEY AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 08/605
REFERENCE/DOCKET NUMBER: 8484-00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOEPRY DISK
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09430010 Patent No. 6395512
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(650)493-5556
                                                                                                                                                                                                          Query Match 2.4%;
Best Local Similarity 57.1%;
Matches 52; Conservative
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650)493-5556
TELEX: 66141 PENNIE
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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                                                               TOPOLOGY: linear MOLECULE TYPE: DNA FEATURE:
                                                                                                                            ; NAME/KEY: CDS
; LOCATION: 1 ...
US-08-578-634C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-430-010-2
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Patent No. 6025163
GENERAL INFORMATION:
APPLICANT: Vladimit Shamanin
APPLICANT: Ethel Michele De Villiers
APPLICANT: Erne Leigh
APPLICANT: Trene Leigh
APPLICANT: Harald Zur Hausen
TITLE OF INVENTION: UND CODING FOR A PEPTIDE OF A PAPLILOMA
TITLE OF INVENTION: VRUS MAIN CAPSIDE PROTEIN AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                  Length 25165;
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Pred. No. 1.2e+02;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                               NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 25165
                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-453-702B-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4155 GATGATTTGCGCCTGAGCATGTTCC 4131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 GGAGACTGACGCTTCAGCCAGTACC 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Pennie & Edmonds LLP
1155 Avenue of The Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/578,634C FILING DATE: 26-JAN-1996 PCLASSIFICATION: 435 PCLASSIFICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Abrams, Samuel B. REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8484-007
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-08-578-634C-2
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910 ACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTTTTGTCTGACAA 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Irene Leigh
APPLICANT: Harsen
TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA
TITLE OF INVENTION: URUS MAIN CAPSIDE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 9
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                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/430,010
Score 28.6; DB 3;
Pred. No. 19;
0; Mismatches 39;
                                                                                                                                                                                                            970 TAGTGAAGCGGTGACAGCATATCAGACGCCT 1000
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226 CAATGATCTGTGCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGG 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 CTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAGTGCGCCGGTCCATG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 CAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 2563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /product Partial Sensor Coding OTHER INFORMATION: Sequence US-08-608-241-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witchuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FOI
TITLE OF INVENTION: SENSING AND REMEDIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4%; Score 28.6; DE 47.1%; Pred. No. 43; tive 0; Mismatches
                 ATTORNEY AGENT INFORMATION:
NAME: Seay, NICholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEFAX: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Rhodobacter sphaeroides
STRAIN: 2.4.1
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/922,182
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Patent No. 5834300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
^AMDITER: IBM PC compatible
PC compatible
PC -DOS/MS
                                                                                                                                                                                                              LENGTH: 2563 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 47.1 Matches 88; Conservative
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 2113..2400
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles &
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APPLICANT: Donohu
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    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Madison
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US-08-922-182-5
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                                                                                                                                                                  240 ACTGGTAAATACTGTAATAGAAGATGGAGATATGGTGGATATAGGTTTTGGAAATATAAA 299
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                                                                                     Gaps
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                                           Length 668;
                                       Score 28.6; DB 4; Length 60
Pred. No. 19;
0; Mismatches 39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Yu, Su-May
TITLEANT: CHOOMOTER
FILE REFERENCE: 08919-047001
CURRENT APPLICATION UNMERR: US/09/575,574
CURRENT FILIG DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            936 GTCTTACGGGTGATGTAGGTTTTTTGTCTGACAATAGTG 974
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIALS
COMPUTER: IBM PC COMPATIALS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,241
FILING DATE:
                                                                                                                                                                                                            970 TAGTGAAGCGGTGACAGCATATCAGACGGCT 1000
                                                                                                                                                                                                                                    300 TAATAAAACCCTGTCAGCAAATAAGTCAGAT 330
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STREET: 1 South Pinckney Street
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                                                                                                                                                                                                                                                                                                                   RESULT 43
US-09-575-574-5
Sequence 5, Application US/09575574;
Patent No. 6376750
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1 Similarity 55.6%;
55; Conservative
                                     Query Match
Best Local Similarity 57.1:
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-575-574-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Donohue
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US-09-430-010-2
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Best Local
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226 CAATGATCTGTGCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGG 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 CAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 2113..2400
OTHER INFORMATION: /product- "Partial Sensor Coding
OTHER INFORMATION: Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Yu, Su-May
APPLICANT: Yu, Su-May
TILLE OF INFORMATION: PLANT SEEDLING AND EMBRYO PROMOTER
FILE REFERENCE: 08919-047001
CURRENT APPLICATION NUMBER: US/09/575,574
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28.6; DB 2;
Pred. No. 43;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rhodobacter sphaeroides STRAIN: 2.4.1
                                        US/08/919,953
                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09575574
Patent No. 6376750
                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 960.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPHONE: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTER.FSTICS:
LENGTH: 2563 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.4%;
Best Local Similarity 47.1%;
Matches 88; Conservative (
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1029 TCCGCCC 1035
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                                                                                                                                                                                                                                                                                                                                                                                                             linear
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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                                                                                                                                               FILING DATE:
                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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LENGIH: 3572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 CAGACACCCCCCCCCCCCCGGGTAACAGCGTCCCTGTCATTCTTCTGAATGACATCAGGGA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             849 CGAGCAGCTGAACGGGAATGCATGTATGCATGTGAACCAGACCATGACCGGGGTCGCGAT 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 CTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCCAGTGCGCCGGTCCATG 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 2563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Withthun, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FOI
TITLE OF INVENTION: SENSING AND REMEDIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28.6; DB
Pred. No. 43;
0; Mismatches
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 15.51-9166
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          South Pinckney Street
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08919953
Patent No. 5837481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.4%;
Best Local Similarity 47.1%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                          LENGTH: 2563 base pairs
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                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
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Length 2563; Indels us-09-674-277-2.rni

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FILING DATE:
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APPLICANT: MUKUMOTO, Fujio
APPLICANT: MUKUMOTO, Shoichi
APPLICANT: MUKUMOTO, Shoichi
APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: DNA Fragments Containing Biotin Biosynthetase Gene and
TITLE OF INVENTION: Use of the Same
TITLE OF INVENTION: Use of the Same
FILE REFERENCE: 0152-0490P
CURRENT APPLICATION NUMBER: US/09/180,109A
CURRENT FILING DATE: 1988-12-03
PRIOR PILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 621
                                                                                                                 876 ATCATGGGTGAGATAGGCACAACAATGAAATCACACAGATAATTCAGGGAAAACGTTCTG 935
                                                                                                                                                        343 ATCATGGATTAATTAGGCTCAATAGATTTGTCTCGCGAATTAGTCCGAGATTATGGATGA 402
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                                        DB 4; Length 3572;
                                  Ouery Match 2.4%; Score 28.6; DB 4; Length 3 Best Local Similarity 55.6%; Pred. No. 52; Matches 55; Conservative 0; Mismatches 44; Indels
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Pred. No. 22;
0; Mismatches 31; Indels
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Patent No. 5668004
GENERAL INFORMATION:
APPLICANT: Michael E. O'Donnell
TITLE OF INVENTION: DNA POLYMERASE III
TITLE OF INVENTION: HOLOENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Strain = JCM7511
; NAME/KEY: CDS
; LOCATION: (1)..(618)
US-09-180-109A-17
                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09180109A
Patent No. 6410293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Sphingomonas paucimobilis
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CORRESPONDENCE ADDRESS:
ADDRESSE: Talwark & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
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Best Local Similarity
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GENERAL INFORMATION:
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US-09-180-109A-17/c
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GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael
TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
FILE REFERENCE: 19603/10214
CURRENT APPLICATION NUMBER: US/08/828,323A
CURRENT FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 29;
0; Mismatches
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Pred. No. 29;
0; Mismatches
                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,058B
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                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEORGE M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF I
TELECOMMUNICATION INFORMATION:
TELEFRAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.4%;
Best Local Similarity 50.0%;
Matches 71; Conservative
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Best Local Similarity 50.0%;
Matches 71; Conservative (
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ORGANISM: Escherichia coli
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STRANDEDNESS: single
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US-08-279-058B-13
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574 GCAATGCGGCAAGTAATGCATC 553

Search completed: June 19, 2003, 03:36:30 Job time: 73.8861 secs

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                                                                                            ; Search time 298.567 Seconds (without alignments) 5804.490 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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/cgn2_6/ptcdata/1/pubpna/US60_PUBCOMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-10-270-875-1

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US-10-270-85-1

US-10-270-85-1

US-10-270-85-1

US-09-974-300-1730

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US-09-918-995-8152

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Sequence 33, Appl
Sequence 114, Appl
Sequence 214, App
Sequence 2285, Ap
Sequence 2287, Ap
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Sequence 574, App
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Sequence 574, App
Sequence 674, App
Sequence 674, App
Sequence 612, Appl
Sequence 412, Appl
Sequence 412, Appl
Sequence 260, App
Sequence 260, Appl
Sequence 260, Appl
Sequence 60, Appl
Sequence 60, Appl
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Sequence 61, Appl
Sequence 330, Appl
Sequence 61, Appl
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Sequence 101, Appli
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Sequence 17, Appl
Sequence 3954, Ap
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US-09-974-300-1695/c
; Sequence 1695, Application US/09974300
; Patent No. US20020146721A1
; Patent No. US20020146721A1
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Expression
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT PELLING DATE: 2001-10-05
PRIOR PELLING DATE: 2001-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-06

PRIOR FILING DATE: 2001-06

FRIOR FILING DATE: 2001-06

SOUTHWER OF SEQ ID NOS: 8481

LENGTHRE FASTESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 6118

LENGTH: 783
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4.1%; Score 48.6; DB 10; Length
Best Local Similarity 49.8%; Pred. No. 6.5e-06;
Matches 123; Conservative 0; Mismatches 124; Indels
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1695
LENGTH: 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6118, Application US/09974300 Patent No. US20020146721A1
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; OTHER INFORMATION: n = A,T,C or
US-09-974-300-6118
                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Bacillus licheniformis
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Matches 121; Conserv
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1072 CATCTCCTTTAGGCGTCACCATACCGGTCACATTATGTTCAACGATTTCGGGAAGTCCCC 1013
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Sequence 1, Application US/10270875

Publication No. US2003008241A1

SEREMAL INFORMATION:

APPLICANT: Sigridur Hjorleifsdotter

APPLICANT: Gudmundur O. Hreggyidsson

APPLICANT: Jakob K. Kristjansson

APPLICANT: Arnthor Aevarsson

APPLICANT: Arnthor Aevarsson

APPLICANT: Arnthor Host Organism

FILE REFERENCE: 273.1001-001

CURRENT APPLICATION NUMBER: US/10/270,875

CURRENT APPLICATION NUMBER: US/09/585,858

FRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 73

SOFTWARE FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 129908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 CCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCA 455
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Pred. No. 0.0024;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
FILE REFERENCE: 10085.500-0S
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/279,526
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFFWARE: FRSESEQ for Windows Version 4.0
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60.4%; Pred. No. 0.
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                                                                                                                                                                                                                                                                              ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Bacterlophage RM378
US-10-270-875-1
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Best Local Similarity 62.5%;
Matches 65; Conservative
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Matches 67; Conservative
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LENGTH: 1227
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                                                                          451 TITIGGIIGCCIAGCAIAAGGACAICGIIIGICAAGCCGIIIICIICCACAAACIGCCIC 392
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  631 TICCCAAGGGGGCATAAATAACCAGTTACTICGICTICAACAACTICCGGGAIGCCACCA 572
                                               GTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAAC 473
                                                                                                                                      474 GCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGGTAGACCGGTAACGCTGGG 533
                                                                                                                                                                                   511 CTTTCTTTTCGCTTAACAACAGCATTAAATCGCTCATAGACAACAATTCAGCAACATGC 452
                                                                                                                                                                                                                              3.9%; Score 46.2; DB 10; Length 783; ilarity 59.5%; Pred. No. 4.5e-05; Conservative 0; Mismatches 53; Indels 0
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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500 US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT PILING DATE: 2001-10-05
PRIOR PAPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-77
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
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; NAME/KEY: misc_feature

; LCATION: (1)...(783)

; OTHER INFORMATION: n = A,T,C or G

US-09-974-300-6111
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Matches 78; Conserva
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LENGTH: 783
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SOFTWARE: FastSE
SEQ ID NO 1
LENGTH: 129908
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Pred. No. 0.11;
0; Mismatches 44; Indels 0;
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APPLICANT: Signifur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Arnthor Aevarsson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
CURRENT PRILING PATE: 2002-1001
CURRENT PRILING DATE: 2002-10-11
PRIOR PPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
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                                               APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Coganism
FILE REFERENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/10/270,878
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
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                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
Gudmundur O. Hreggvidsson
Olafur H. Fridjonsson
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                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Bacteriophage RM378
US-10-270-878-1
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Best Local Similarity 60.4%;
Matches 67; Conservative
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PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
                                     Arnthor Aevarsson
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Best Local Similarity
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LENGTH: 129908
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LENGTH: 129908
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                                                                                                                                                                         APPLICANT: Gudmundur O. Hreggyidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjanson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host organism
TITLE OF INVENTION: 10st organism
TITLE OF INVENTION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
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Pred. No. 0.11;
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3.4%; Score 40.6; DE
Best Local Similarity 60.4%; Pred. No. 0.11;
Matches 67; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILLING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                APPLICANT: Sigridur Hjorleifsdotter
Sequence 1, Application US/10270710 Publication No. US20030092128A1 GENERAL INFORMATION:
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Matches 67; Conservation
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US-10-270-710-1
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10181 ATCTGCAATACCACCCGTCATAGTAGCAACCACCGGGGCTCCACACAGCGACGCCTCAAG 10122
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Pred. No. 0.09;
0; Mismatches 60; Indels 0; Gaps
                                                                                                                                 458 CAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGC 508
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Clausen, 1b Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR FILING DATE: 2000-10-06
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APPLICANT: No. US20020137677Alak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHAll CYTOKINE RECEPTORS FILE REFERENCE: 00-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FLIANG DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                               Sequence 1730, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09825561A Patent No. US20020137677A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA CORGANISM: Bacillus licheniformis US-09-974-300-1730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.1%;
Best Local Similarity 54.9%;
Matches 73; Conservative
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1003 GTCCTGCTATATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCC 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1063 CGATAATCCGTCGAAGTCTGAGGATGGAAGGAGGTGAAGGCTGTGTTCCTGAAAGGAATAA 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
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                                                                                                                                                                                                                                                                                                                                                                                                               883 GTGAGATAGGCACAACAATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTAC
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                          a
                                          Degenerate polynucleotide sequence of soluble zalphall Receptor polypeptide as shown in SEQ
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                                                                                                                                                                                                                                                                                          Length 654;
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                                                                                                                                                                                                                                                                                       Query Match 3.1%; Score 36.6; DB 10; Best Local Similarity 30.7%; Pred. No. 0.089; Matches 74; Conservative 35; Mismatches 132;
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PRIOR FILING DATE: 2000-02-04
PRIOR PLILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-03
PRIOR PRILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14748, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
FEATURE:
OTHER INFORMATION: Degenerate polynu
OTHER INFORMATION: zalphall Receptor
OTHER INFORMATION: NO:6
NAME/KEY: mlsc_feature
LOCATION: (1)...(654)
CTHER INFORMATION: n = A,T,C or G
US-09-825-561A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Degenerate polynucleotide sequence of SEQ ID NO:69 NAME/KEY: misc_feature
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Best Local Similarity 56.2%; Pred. No. 0.12;
Matches 68; Conservative 0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
CTHER INFORMATION: EXPRESSED IN FUTAL LIVER, SIGNAL = 0.46
US-09-864-761-14748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Specher, Cindy A.
APPLICANT: No. US20020137677Alak, Julia E.
APPLICANT: No. US20020137677Alak, Julia E.
APPLICANT: West, James W.
APPLICANT: West, James W.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Nolson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHALI CYTOKINE RECEPTORS FILE REFERENCE: 00-22
CURRENT PPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE PASSEG for Windows Version 3.0
SEQ ID NO 66
SEQ ID NO 66
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOCTUMARR: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 14748
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; OTHER INFORMATION: n = A,T,C or G
US-09-825-561A-66
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                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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1095 AATCTTGCGGCTGAGCGGTTCATGAAAACCGATATACGCCTTGCACCTGTCCGGAAAAGC 1036
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                                                                                                                                                                                                                                                                                                              953 GCTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTAT 1012
                                                                                                                                                                                                                                                                                                                                                                                                                    1013 ATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCG 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 GGNAAYTAYWSNCARGARTGYGGNWSNTTYYTNYINGCNGARWSNMGNCARTAYAATH 438
                                                                                                   833 AACCGTTACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGGTGAGATAGG 892
                                                                                                                                                  139 AAYYINCAYCCNWSNACNYINACNYINACNTGGATHYINWSNAAYAAYACNGGNTGYTAY 198
                                                                                                                                                                                                          893 CACAACAATGAAATCACACAGATAATTCAGGGAAAACGTTCTGGTCTTACGGGTGATGTA 952
                                                                                                                                                                                                                                                            199 ATHAARGAYMGNACNYINGAYYINMGNCARGAYCARTAYGARGARYINAARGAYGARGCN 258
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                                                                                                                                                                                                                                                                                                                                                  259 ACNWSNTGYWSNYTUCAYMGNWSNGCNCAYAAYGCNACNACAYGCNACNTAYACNTGYCAY
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  Length 741;
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1D Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 00/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 757
LENGTH: 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 10; Length 14
Pred. No. 0.24;
0; Mismatches 185; Indels
Score 36.2; DB 10;
Pred. No. 0.13;
                                                    48; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 757, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bacillus licheniformis
US-09-974-300-757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.0%;
Best Local Similarity 46.0%;
Matches 160; Conservative
  3.18; 27.68;
                                                       Conservative
     Query Match
Best Local Similarity
Matches 83; Conserv
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; ORGANISM: Bacillus licheniformis US-09-974-300-1702
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                                          1013 ATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCG
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                                                                                                698 TTTTCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAACATTGTC 745
                                                                                                                                      TTTTTGCTTCGTCAGCCTTGCCACCATGCTGAGGGGGAATGTCTTC 871
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                                                                                                                                                                                                                                Sequence 8152, Application US/09918995
Fublication No. US2003007362341
GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.; TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: PROM VARIOUS cDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 30054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NOS 8152
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Fatent No. US20020146721A1
GENERAL INPORMATION:
APPLICANT: Berka Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-77
NUMBER OF SEQ ID NOS: 8481
SOUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1702
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; CCATION: (1)...(480)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8152
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ORGANISM: Homo sapiens
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US-09-918-995-8152/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 YK.SY...MKST.RYMWSBR.B...B.BS...TBSCT..MD.S.D.THTHA..C..ATC
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                                                                                                      352 CATCCCCACGGGTAACAGCGTCCCTGTCACTTCTTCTGAATGACATCAGGGATCCCGC
                                                                                                                                                                                                                412 CCGTCTCACTGGCGATAACGGGCACGCGGAGACTGACGCTTCAGCCAGTACCAAA
                                                          Gaps
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Ouery Match 3.0%; Score 35; DB 10; Length 1135; Best Local Similarity 50.9%; Pred. No. 0.46; Matches 83; Conservative 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 513;
                                                                                                                                                                                                                                                                                                                                                          847 GCCCTTCCCTGATGCTTGAGGCGACAGACACGTCTGCAAGCTG 805
                                                                                                                                                                                                                                                                                                                         472 ACGCTTCATTTCCGAAGGCATGACCACCACACTGGCAATCCG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.9%; Score 34.8; DB 9; larity 6.9%; Pred. No. 0.32; Conservative 115; Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 536, Application US/10123155
Publication No. US20030068794A1
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Smith, Victoria
Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
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US-10-123-155-536
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GENERAL INFORMATION
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190 IGIIGCAITICCCCITAGCCIGACIAGCCAGAGACACAAIGAICIGIGCCGITCIGITAA 249
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291 HY.RCMMN..RN.R...YK.RSWBG.BCT.YYBGYCB.BH.DAARK.Y.GMC.D.BKYY. 232
                                                                                            550 TTAACACATCTCCGCTCATTCCCAGGTGTTCTGTCTGCTGACGCAGGCGTGCTTCGTATT 609
                                                                                                                                             231 B:YSK.BC.CCKG.N.C..T.MCK..AAC.CA.C....SSN.SY..N..YHCM.RBHH 172
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430NG217
CURRENT APPLICATION NUMBER: 105/10/184,634
CURRENT FILING DATE: 2002-06-28
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 312
LENGTH: 802
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5.2%; Pred. No. 0.43;
[ve 170; Mismatches
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Publication No. US20030068684A1
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Wood, William I.
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Gurney, Austin L.
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gurdey, Austin L.
APPLICANT: Gurdey, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watenable, Colin K.
APPLICANT: Applicant: Applicant: Colin K.
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             N.BG.,BS:CS.T...NCS.H.Y..SSWAWSKA.C.BS.MNW..R.N..SB.Y...T.N. 220
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Pred. No. 0.43;
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Chen, Jian
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :| :: :: | : :: | : | . | . | . | | . | | . | | . | | . | | . | | . | | . | | . | | . | | . | | . | | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 GCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCAATCCGG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 C-..HN...WHR.YANTC.AS.MMCMRYW.BM....T.TST..NTM..ABN...SC.S.B 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 TAGACCGGTAACGCTGGGAAAAGGGCACCTGCCATTAACACATCTCCGCTCATTCCCAGG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227 CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT FILING DATE: 2002-06-28 Prior Application removed - See File Wrapper or Palm NUMBER 05 SEQ ID NOS: 612 LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 CCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 KM.ACY..B..HN.M.BS.WAS.C..BN.T.HB...N..AYH..KDBB..M.TS.MYRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AAAATTCGGGCTGAAAAGAGGATCCGCCGTTATCTGTTGCATTTCCCCTTAGCCTGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430HIC217 CURRENT APPLICATION NUMBER: 105/10/184,634 CURRENT FILLING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 GCCAGAGACACAATGATCTGTGCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 .S.MSDA.BAB.DCYB.....BMBN.WDSKHG.WB.BMCG.C 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

2.9%; Score 33.8; DB 9;
Best Local Similarity 9.9%; Pred. No. 0.73;
Matches 46; Conservative 134;. Mismatches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 522, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe, Colin
Wood, William I.
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Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
          Zhang, Zemin
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                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo Sapien
US-10-184-644-522
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TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLOO0871 DIV

CURRENT PAPLICATION NUMBER: US/10/274,974

CURRENT FILING DATE: 2002-10-18

PRIOR APPLICATION NUMBER: 60/182,194

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 74962
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                                                                                                                                                                                             171 HTYK.W.RMH.RDHDKRW.KK.SMM...RSHHBCY..BB...BSAHSC.SS...BMC..A 112
                                          231 B.YSK.BC.CCKG.N.C..T.MCK..AAC.CA.C....SSN.SY..N..YHCM.RBHH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AGCTGAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 CAATGTGATAAATTACTCCGTTACCGGAAAACCGCTGAACAAATTCGGGCTGAAAAGAG 175
550 TTAACACATCTCCGCTCATTCCCAGGTGTTCTGTCTGCTGACGCAGACGTGCTTCGTATT 609
                                                                                                                                       CTTCACGCCCGGCCCCACCACGAGCCAGCGAATGATTTCCCTTCCATCTTCAGCTGAT 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                    670 ACAATACACGCAGCATAAATTCATGTCCTTTTTCGGGACGTAGCATCCCCACCT 723
                                                                                                                                                                                                                                                                                                        111 MSWAYRTIBIYA..RM.TAKBCB...NYHY.CCH.HSC..W..TCYTHCYTCCT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 74962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.2;
Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5691 GAAACTCTGTCATTTGTGACAAT 5713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 GATCCGCCGTTATCTGTTGCATT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 522, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LCCATION: (1)...(74962)
; OTHER INFORMATION: n = A,T,C or G
US-10-274-974-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10274974 Publication No. US20030054490A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.9%;
Best Local Similarity 52.4%;
Matches 75; Conservative
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 21
US-10-184-644-522/C
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1013 ATTACTGTCATGGCCACTATGGCAGATGACCAGATCAGGTTTAAATTCCCCGATAATCCG 1072
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1073 TCGAAGTCTGAGGATGGAAGGAGGTGAAGGCTGTTCCTGAAAGGAATAAAAGTGACATC 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 CTTAAACCAGAGTTCATAAGCTTGATGAGTATGATAAAAAGATGTTCATCATGGATTTT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 CTTAAACCAGAGTTCATAAGCTTGATGAGTTATGATAAAAAGATGTTCATCATGGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U32989
US-09-880-107-3347
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Scherf, Uwe APPLICANT: Scherf, Uwe APPLICANT: Scherf, Uwe TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR PILING DATE: 2000-06-14 PRIOR PILING DATE: 2000-06-14 PRIOR APPLICATION NUMBER: US 60/237,054
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Pred. No. 1.6;
0; Mismatches
                                                                                                                                                                                                                          Sequence 3347, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: VOCKLEY, Joseph G.
APPLICANT: Scherf, Uwe
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NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 53.4%;
Matches 71; Conservative
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                                                                               1133 ATGCCCTCTTTT 1145
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Watanabe, Colin K
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Beresini, Maureen
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235 ATTTCCTTTTGTT 223
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Filvaroff, Ellen
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US-09-880-107-3347/c
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE REPERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
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                                                                                                                                              Length 527
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 3507970CB1
US-10-044-090-362
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                                                                                                                                                                    Pred. No. 0.73;
14; Mismatches 282;
                                                                                                                                              Score 33.8; DB 9;
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; Pred. No. 1.5;
0; Mismatches
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                                                                                                                                              Query Match 2.9%; Soc
Best Local Similarity 9.9%; Prec
Matches 46; Conservative 134;
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Best Local Similarity 53.4%;
Matches 71; Conservative
    NOS: 612
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                                                                                      ; ORGANISM: Homo Saplen
US-10-184-634-522
    NUMBER OF SEQ ID
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                       SEQ ID NO 522
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US-10-184-634-348/c
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              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333081C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT APPLICATION NUMBER: US/10/123,155
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                     343 ATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAG
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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US-10-123-155-96
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                                                                                                                                  SEQ ID NO 96
LENGIH: 716
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Matches 42; Conservative 179; Mismatches 342;
                                                                                                                                                                                                                                                                                DB 9;
TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227 CURRENT APPLICATION NUMBER: US/10/184,644 Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 612 SEQ ID NO 348 ENGTH: 777
                                                                                                                                                                                                                                                                             2.8%; Score 33.2; 7.5%; Pred. No. 1.5
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Publication No. US20030068684A1
GENERAL INFORMATION:
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Wood, William I.
Zhang, Zemin
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                                                                                                                                                                                                         ; ORGANISM: Homo Sapien
US-10-184-644-348
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Wood, William
                                               Tumas, Daniel
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US-10-123-155-306
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; ORGANISM: HOMO
US-09-918-995-5997
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LENGTH: 690
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217 CURRENT APPLICATION NUMBER: US/10/184,634 CURRENT FILING DATE: 2002-06-28 Pilor Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                    Length 777;
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Best Local Similarity 7.5%; Pred. No. 1.5;
Matches 42; Conservative 179; Mismatches 342;
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
Gao, Wei-Qiang
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                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapien
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                                                                                                              SEQ ID NO 348
LENGTH: 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 GGATAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 GSADA. NSRA..GC. SSWSCNKAH. SRNW.TG. SYRYHABMYDS.A.A.M...R.A..NS
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                                                                                                                                                  TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; Publication No. US2003007362341
; GENERAL INCORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FESTSEQ for Windows Version 3.0
; SEQ ID NO 5997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 690;
                                                                                                                                                                                                                                                                                                       Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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Best Local Similarity 9.8%; Pred. No. 1.7;
Matches 32; Conservative 100; Mismatches 195;
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                                                                                                                                                                            TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30 CURRENT APPLICATION NUMBER: US/10/123,155 CURRENT FILING DATE: 2002-04-15
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                                                                                                                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND
TITLE OF INVENTION: ACIDS ENCODI
Stewart, Timothy A.
                                                          Watanabe, Colin K
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- See File Wrapper or Palm

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Prior Application removed
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 414
LENGTH: 811
                                                                                           ; ORGANISM: HOMO
US-10-184-644-414
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LENGTH: 811
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                                     Sequence 9370, Application US/10198846
| Publication No. US2003009974A1
| GENERAL INFORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Lillie, James
| APPLICANT: Lillie, James
| APPLICANT: Steinmann, Kathleen
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| CURRENT APPLICATION NUMBER: US/10/198,846
| CURRENT FILING DATE: 2002-07-18
| PRIOR FILING DATE: 2001-07-18
| PRIOR FILING DATE: 2001-07-18
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                                                                                         418 CACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAAC 473
                                                                                                                             262 CATCAGCACCATTGGCCAGGCCTTCGAGTTGCGCTTCAAACAATACCTCACGAACC 317
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Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: 15, 17, 27, 62, 165, 441, 544, 600
; CHER INFORMATION: n = A,T,C or G
US-10-198-846-9370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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FILE REFRENCE: P3430R10227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14084
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9370
LENGTH: 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 414, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
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Goddard, Audrey
Godowski, Paul J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 54.29
Matches 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                      US-10-198-846-9370
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APPLICANT:
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APPLICANT:
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996 CGCTCAGTCCTGCTATATTACTGTCATGCCACTATGCCAGATGACCAGATCAGGTTTA 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663 ILICLYESYFDPGKSISENIVSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS 722
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                                                                                                                                                                                                                                                                                                                     876 ATCATGGGTGAGATAGGCACAACAATGAAATCACACACATAATTCAGGGAAAACGTTCTG 935
                                                                                                                                                                                                                                                                                                                                                                                                                              936 GTCTTACGGGTGATGTAGGTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGA 995
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                                                                                                                                                                                                                                                                                                                                                      543 MAVGWSDSYTCEYPLNLRGTRLKDVHLHELSCNTALLLVTIVVIMLVLGLAVAFCCLHFD
                                                                                                                                                                                                               816 TCGAAACCCGGTGGAATAACCGTTACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCC
                                                                                                                                                                                                                                                           483 GCSHFSRLSVLNIEMNFILSPSLDFVOSCOEVKTLNAGRNPFRCTCELKNFIQLETYSEV
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                                                         Gaps
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                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - See File Wrapper or Palm
Query Match
2.7%; Score 32.4; DB 9;
Best Local Similarity 7.3%; Pred. No. 3;
Matches 25; Conservative 97; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Mismatches 219;
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Wood, William I.
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Best Local Similarity 7.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 GCSHFSRLSVLNIEMNFILSPSLDFYQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEV 542
                                                                                                                543 MAVGWSDSYTCEYPLNIRGTRIKDVHLHELSCHTALLIVTIVVIMLYLGLAVAFCCLHFD 602
                                                                                                                                                      936 GICTTACGGGTGATGTAGGTTTTTTGTCTGACAATAGTGAAGCGGTGACAGCATATCAGA 995
                                                                                                                                                                                                                                                      663 ILICLYESYFDPGKSISENIVSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS 722
                 816 TCGAAACCCGGTGGAATAACCGTTACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCC 875
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                                                                                    876 ATCATGGGTGAGATAGGCACAACAATGAAATCACACAGATAATTCAGGGAAAACGTTCTG
                                                                                                                                                                                  603 LPWYLRMIGQCTQTWHRVRKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGS
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Pred. No. 16;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6047
TEMOTH: 11649
TYPE: DNA
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
CURRENT APPLICATION
UNBER: US/10/091,438
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,879
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6047, Application US/09764891 Publication No. US20030077808A1 GENERAL INFORMATION:
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Sequence 272. Application US/10091438

Publication No. US20030077606A1

; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/180,628
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Best Local Similarity 48.99
Matches 87; Conservative
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R FILING DATE: 2000-11-01
R PILING DATE: 2000-18-18
R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/236,368
R APPLICATION NUMBER: 60/236,856
R APPLICATION NUMBER: 60/251,856
R FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/241,785
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/244,617
FILING DATE: 2000-11-01
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FILING DATE: 2000-09-25
APPLICATION NUMBER: 60/229,343
FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/228,924
FILING DATE: 2000-08-30
APPLICATION NUMBER: 60/224,518
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/236,369
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APPLICATION NUMBER: 60/220,964
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APPLICATION NUMBER: 60/241,809
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APPLICATION WUMBER: 60/249,299
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327
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APPLICATION NUMBER: 60/229,344
                                                                                                                                                                                                           APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
APPLICATION NUMBER: 60/225,757
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/226,868
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APPLICATION NUMBER: 60/225,270
FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/234,274
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APPLICATION NUMBER: 60/234,223
                                                                                                                 APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
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APPLICATION NUMBER: 60/216,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/251,869
                                                                  APPLICATION NUMBER: 60/220,963
FILING DATE: 2000-07-26
                                                                                                                                                                APPLICATION NUMBER: 60/225,447
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/216,647
FILING DATE: 2000-07-07
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APPLICATION NUMBER: 60/235,834
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ILING DATE: 2000-07-11
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APPLICATION DATE: 2000-10-13
A APPLICATION NUMBER: 60/239,937
R FILING DATE: 2000-10-13
R APPLICATION NUMBER: 60/241,787
"TITING DATE: 2000-10-20
              R FILING DATE: 2000-09-05

R APPLICATION NUMBER: 60/236,367

R APPLICATION NUMBER: 60/237,039

R FILING DATE: 2000-10-02

R APPLICATION NUMBER: 60/237,039

R FILING DATE: 2000-10-02

R APPLICATION NUMBER: 60/236,370

R APPLICATION NUMBER: 60/236,802

R R FILING DATE: 2000-00-02

R PILING DATE: 2000-10-02

R PILING DATE: 2000-10-02

R R PLING DATE: 2000-10-02

R R PLING DATE: 2000-10-02

R APPLICATION NUMBER: 60/237,037

R APPLICATION NUMBER: 60/237,040

R R FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/249,216
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,210
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
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APPLICATION NUMBER: 60/225,759
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/225,213
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FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/239,935
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PPLICATION NUMBER: 60/246,474
ILING DATE: 2000-11-08
PPLICATION NUMBER: 60/246,532
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PPLICATION NUMBER: 60/235,836
ILING DATE: 2000-09-27
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FILING DATE: 2000-06-30
APPLICATION NUMBER: 60/225,266
FILING DATE: 2000-08-14
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FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/249,208
FILING DATE: 2000-11-17
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PPLICATION NUMBER: 60/225,214
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3931 TCTCTTCTTTCTCTTCCCTGTCTTATACACTCACCCTATATAAGTCATTTCTCTAA 3990
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Best Local Similarity 48.9%; Pred. No. 16;
Matches 87; Conservative 0; Mismatches
          PRIOR FILING DATE: 2000-11-17
PRIOR PELICATION NUMBER: 60/249,214
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR PLING DATE: 2000-11-17
PRIOR PELING DATE: 2000-19-08
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R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,297
R FILING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/232,400
TITTAG DATE: 2000-09-14
PELICATION NUMBER: 60/249, 264
LING DATE: 2000-11-17
PELICATION NUMBER: 60/249, 214
LING DATE: 2000-11-17
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; Sequence 90, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Otang
APPLICANT: Gerittsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
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1154 TGTTCGACGGCGTCTTCACCCATTCTGATGCGCGTTTCGTCATCGTCCAAGAGTGTGGCT 1095
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                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                      Score 32.2;
Pred. No. 4.
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PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR PELICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR PRILING DATE: 2001-05-27
PRIOR FILING DATE: 2001-05-27
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DAFE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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PRIOR FILING DATE: 2001-06-13
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                                                                                                                                                                                                                                            ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-451
                                                                                                                                                                                                                                                                                                                      2.78;
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IG DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Castle, Arthur
: Elashoff, Michael
: Gene Logic, Inc.
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Matches 115; Conservative
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                                                                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 468;
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2.7%; Score 32.2; DD 9;
Best Local Similarity 7.0%; Pred. No. 2.4;
Matches 27; Conservative 117; Mismatches 241;
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Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                              Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NAKAGAWA, SATOSHI
                                                                                               Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                    Smith, Victoria
                                                                                                                                                                                                                                                                                                          Prior Application removed .
NUMBER OF SEQ ID NOS: 550
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US-10-123-155-90
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424911 GCGACTGCGATGGGCAGGCCGCCAACCCGGGCCGCAATGACCGGTGTGCCGCTGGCTTGC 424852
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                                                   450 GCTTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACACTGGCA
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APPLICANT: Yau, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYCES
CURRENT PELITYRA.011A
CURRENT PELICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SUFFWARE FALSERO FOR WINDOWS VERSION 4.0
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Pred. No. 5.6;
0; Mismatches 85;
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                                                                                                                                                                                                                                                                                                            Sequence 4609, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Staphylococcus aureus US-09-815-242-4609
                                                                                                                                                                          424791 GCCCGATACACGG 424779
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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Best Local Similarity 49.4%;
Matches 83; Conservative
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APPLICANT: Haselbeck, Robert
                                                                                                                                            510 ATCCGGTAGACCG 522
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US-09-815-242-8107/c
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APPLICANT:
APPLICANT:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                       270 TCTTCTCTGGCGCTGGCTGCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGC 329
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                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                       ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022403
US-09-917-800A-1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3309400;
                                                                                                                                                                                                            Query Match 2.7%; Score 32.2; DB 10; Length 1689; Best Local Similarity 52.6%; Pred. No. 5.6; Matches 70; Conservative 0; Mismatches 63; Indels 0;
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Best Local Similarity 45.5%; Pred. No. 3.5e+02;
Matches 115; Conservative 0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PAPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: MIXOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || |||| | || || || || 231 ATTCCCTTTGATT 219
                                                                     TYPE: DNA ORGANISM: Rattus norvegicus
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SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1734
LENGTH: 1689
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APPLICANT:
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388 Y.B.A.G.RMYINYDA.GN..T...H..TMN.SCMAIR.TCYTB.T.BN.MH...TMNR. 329
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                                                                                                                                                                                                                                                                                                                                    290 CATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCCGGTGCGCCGGTCCATGCAGA 349
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 M.R., YH.MC., M.B., MDN., STSANT, B.RG.HMYN.H., NSSTYSSDSYSSYSS, SY
                                                                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 5.8%; Pred. No. 4.2;
Matches 34; Conservative 186; Mismatches 370; Indels
                                                      Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 402
                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                              Score 31.8;
                   US/10/184,644
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                                        2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney, Austin L
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Wood, William I.
                   CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2002-0
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Goddard, Audrey
REFERENCE: P3430R1C227
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                                                                                                                                                                                ) ORGANISM: Homo Sapien
US-10-184-644-402
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US-10-184-634-402/C
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APPLICANT:
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                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693 TGTCCTTTTTCGGGACGTAGCATCCCCACCTGAACGATAAGCGGAACATTGTCTGCTGAT 752
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633 AGCCAGCGAAATGATTTCCCTTCCATCTTCAGCTGATACAATACACGCAGCATAAATTCA
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                                                                                                                                                                                       Genes
                                                                                                                                                                                       Essential
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                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                     TITLE OF INVENTION: Identification of TITLE OF INVENTION: Prokaryotes
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Publication No. US20030044930A1
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                                                                                                                    Carr, Grant J.
Yamamoto, Robert T.
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                            Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William I.
Zhang, Zemin
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Best Local Similarity 49.4*
These B3; Conservative
                                                                                               John D.
                                                                                                                                                                                                                               FILE REFERENCE: ELITRA.011A
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Smith, Victoria
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APPLICANT: Baker, Kevin P.
                                                                                                                                                                    Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (1)...(1563)
US-09-815-242-8107
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                                                                                                 Trawick,
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APPLICANT:
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LENGTH: 1049
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                                                                                                                                                                                                          290 CATCATCCGGAAGCGTTCCGGTCGGGATAAAAATCGCGCAGTGCGCCGGTCCATGCAGA 349
                                                                                                                                                                                                                                                            CACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTGAATGACATCAGGGATCCC 409
                                                                                                                                                                                                                                                                                                               GCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACC 469
                                                                                                                                                                                                                                                                                                                                                                                                                   590 ACGCAGACGTGCTTCGTATTCTTCACGCCCGGCGCCCACCACGAGCCAGCGAAATGATTT 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          770 ATGCAGGGTAACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGG 829
                                                                                                                                                                                                                                                                          568 M.R..YH.MC..M.B..MDN..STSANT.B.RG.HMYN.H..NSSTYSSYSSYSSYSY
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                                                                                                                                                       2.7%; Score 31.8; DB 9; Length 6 ilarity 5.8%; Pred. No. 4.2; Conservative 186; Mismatches 370; Indels
TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217 CURRENT APPLICATION UNMBER: US/10/184,634 CURRENT FILING DATE: 2002-06-28 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 402 LENGTH: 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 358, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers, Luc
Filvaroff, Ellen
Gao, Wet-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DeForge, Laura
                                                                                                                ; ORGANISM: Homo Sapien
US-10-184-634-402
                                                                                                                                                                    Similarity
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                                                                                                       TYPE: PRT
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Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Sherwood, Steven Gerritsen, Mary E.

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Sequence 35, Application US/09891641
Patent No. US20020155612A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Tao
APPLICANT: Wang, Tao
TITLE OF INVENTION: NATURAL PROMOTERS FOR GENE EXPRESSION IN BACILLUS SPECIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BS.H.BM.YM..M.KS.NT.M..NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.S 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...NM.SYSGNS.Y..BAA..NDS.H.A..NM.G..MMWS.SM.CNWT.S.NM.N..KCH
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                                                                             APPLICANT: Watenabe Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
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                                                                                                                                                                                                                                                                                                              Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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Matches 23; Conservative 151; Mismatches 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%; Score 31.8;
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/123,155 CURRENT FILING DATE: 2002-04-15
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Smith, Victoria
Stewart, Timothy A.
                                                        Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapien
US-10-123-155-358
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APPLICANT: HOLTZMAN, Douglas A.
APPLICANT: FRASER, Christopher C.
APPLICANT: SHARP, John D.
APPLICANT: SHRAP, John D.
APPLICANT: SHRAP, John D.
APPLICANT: HOLTZMAN, DOUGLES S.
TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTH
FILE REPERBNGS: 10147-1103
CURRENT APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-60-16
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 100
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000 ACTCCACCGTGGCTGGCACTGGCGAGCACTGGCTGGGCCTGCACTGAGGTGCCT 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 GCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACCACCACTGGCAATCCGG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 ACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCA
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Pred. No. 11;
0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 3153;
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                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
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2.7%; Score 31.8; Di
Best Local Similarity 51.0%; Pred. No. 11;
Matches 75; Conservative 0; Mismatches
    PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR PRILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 343
LENGTH: 3153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1880 GGGCCCATGTAGCTGGAAGTAGGGAA 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 TAGACCGGTAACGCTGGGAAAAGGGCA 542
APPLICATION NUMBER: US 09/393,996
FILING DATE: 1999-09-10
APPLICATION NUMBER: US 09/602,871
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; sequence 73, Application US/10189123
; Publication No. US20030082586A1
; GENERAL INFORMATION:
; APPLICANT: KIRST, Susan J.
                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1)...(3153)
; OTHER INFORMATION: n = A,T,C or G
US-09-759-130B-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.7%;
Best Local Similarity 51.0%;
Matches 75; Conservative (
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SEQ ID NO 73
LENGTH: 3153
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LOCATION: (3048)...(3048)...
OTHER INFORMATION: unknown
US-10-189-123-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (3043)..(3043)
OTHER INFORMATION: unknown
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LOCATION: (3043)..(304)
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                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mus sp.
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 GAIGATTICCCGATGCCCGCGATTAICTGTGGCGATCGCCGGTTGTTCTGCCGCCATTCC 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 TTCAGCCAGTACCATACCAAACGCTTCATTTTCCGAAGGCATGACCACACACTGGCAAT 511
                                                                                                                                                                                                                                                                                                                                                 272 INCICIGGCGCTGCCTCCATCATCCGGAAGCGTTCCGGTCGGGATAAAAAATCGCGCAG 331
                                                                                                                                                                                                                                                                                                                                                                                392 AATGACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCCGGAGACTGACGC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 IGCGCCGGTCCATGCAGACACATCCCCCACGGGTAACAGCGTCCCTGTCACATTCTTCTG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990 CCGGCGGCAAAAAGCAGCACTGTCACGATTTTGATCAGAAAACCGTTTTCTCCGTCGGC 931
                                                                                                                                                                                                                                                                                                         Gaps
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0
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Pred. No. 6;
0; Mismatches 132;
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APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE CEFERENCE: MPIOO 5350MNIM CURRENT APPLICATION NUMBER: US/09/759,130B CHRRENT FILING DATE: 2002-09-16
       FILE REFERENCE: CL1686 US NA
CURRENT APPLICATION NUMBER: US/09/891,641
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft 97
SEQ ID NO 35
LENGTH: 1146
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PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR PRILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PLICATION NUMBER: US 09/342,364
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APPLICATION NUMBER: US 09/608,452
FILING DATE: 2000-06-30
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APPLICATION NUMBER: US 09/559,497
FILING DATE: 2000-04-27
APPLICATION UNMBER: US 09/578,063
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PRIOR APPLICATION NUMBER: US 09/479,249
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Myers, Paul S
Leiby, Kevin R
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                                                                                                                                                                         TYPE: DNA
COGGANISM: Bacillus subtilis
US-09-891-641-35
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Best Local Similarity 45.7
Matches 111; Conservative
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                        CCCAGGCGTGGATATGCAGGGGTAACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430HZB17 US/10/184,634
CURRENT APPLICATION NUMBER: 2002-06-28
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2.7%; score 3.1.v, ...,
Best Local Similarity 6.5%; Pred. No. 5;
Matches 33; Conservative 171; Mismatches 302;
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pred. No. 5;
                                                                                                          817 CGAAACCCGGTGGAATAACCGTTACC 842
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                                                                                                                                                                                                                                                          Sequence 346, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
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Gurney, Austin L.
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Goddard, Audrey
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Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-184-634-346
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APPLICANT:
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                        APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zenin
APPLICANT: Zhang, Zenin
TITLE OF INVERTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVERTION: ACIDS ENCODING THE SAME
TITLE OF THE PRINCE: P349181227;
CURRENT APPLICATION NUMBER: US/10/184, 644
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ACATCAGGGATCCCGCCCGTCTCACTGGCGATAACGGGCACGCGGGAGACTGACGCTTCA 455
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NUMBER OF SEQ ID NOS: 612
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Best Local Similarity 6.5%; Pred. No. 5;
                                                                                                                                                                    516 TAGACCGGTAACGCTGGGAAAAGGGCA 542
                                                                                                                                                                                                                                                                                                                      Sequence 346, Application US/10184644 publication No. US20030044930A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
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ORGANISM: Homo Sapien
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2478 GCCCGTGCGACATGCGATGACGGCTTGCCTGCGTGCAAGGCCTCTGAAACCTTTACTTC 2419
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Pred. No. 13;
0; Mismatches 119;
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Job time: 311.567 secs
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Best Local Similarity 46.4%;
Matches 103; Conservative
                      PatentIn version 3.0
                                                                                                                   ORGANISM: Grifola frondosa
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NAME/KEY: terminator
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SOFTWARE: Pater
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LENGTH: 2817
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Patent No. US20020068349A1
GENERAL INFORMATION:
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TITLE OF INVENTION:
TREHALOSE PHOSPHORYLASE, VECTOR CONTAINING THE GENE
TITLE OF INVENTION:
TREHALOSE PHOSPHORYLASE, AND METHOD FOR PRODUCING F
TITLE OF INVENTION:
TREHALOSE PHOSPHORYLASE WITH THE USE OF TRANSFORMANT
                                                                                                                                                                                                                                                                                                                APPLICANT: Saitoh, Kohki
APPLICANT: Takahashi, Eisaku
TITLE OF INVENTION: GENE ENCODING TREHALOSE PHOSPHORYLASE, VECTOR CONTAINING THE GENE
TITLE OF INVENTION: GENE ENCODING TREHALOSE PHOSPHORYLASE, AND METHOD FOR PRODUCING R
TITLE OF INVENTION: TREHALOSE PHOSPHORYLASE WITH THE USE OF TRANSFORMANT
FILE REFERENCE: FJIN-100
CURRENT APPLICATION UNMBER: US/09/381,624A
CURRENT FILING DATE: 1999-12-15
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     222 CC..CYY.TYBTTMM..A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTMYTYMSBSKM 163
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Pred. No. 11;
0; Mismatches 119;
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CURRENT APPLICATION NUMBER: US/09/381,624A
CURRENT FILING DAFE: 1999-12-15
PRIOR APPLICATION NUMBER: US 09/381,624
PRIOR FILING DATE: 1999-12-15
                                                    817 CGAAACCCGGTGGAATAACCGTTACC 842
                                                                                  162 .T.AMYM.CSNHSSMHSHSHS.KYHS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/381,624 PRIOR FILING DATE: 1999-12-15
                                                                                                                                                                                                                   Sequence 5, Application US/09381624A Patent No. US20020063349Al GENERAL INFORMATION: APPLICANT: Horinouchi, Sueharu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.78;
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Best Local Similarity 46.45
Matches 103; Conservative
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| NAME/KEY: terminator
| LOCATION: (2197)..(2199)
| US-09-381-624A-5
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US-09-381-624A-4/c
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